

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 26.813 Seconds  
(without alignments)  
1008.352 Million cell updates/sec

Title: US-10-662-429-2  
Perfect score: 1478  
Sequence: 1 MAMMEVQGSLGTCVTLV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189.5	12.8	279	2 A53062	Fas ligand - mouse
2	186	12.6	281	2 I38707	Fas ligand - human
3	177.5	12.0	278	2 A49266	Fas ligand - rat
4	164	11.1	261	2 S53090	CD40 ligand - bovi
5	147.5	10.0	261	2 I53476	CD40 ligand - huma
6	141	9.5	234	1 A25451	tumor necrosis fac
7	141	9.5	260	2 S21738	CD40 ligand - mous
8	134.5	9.1	204	1 S17289	tumor necrosis fac
9	133	9.0	232	1 S12606	tumor necrosis fac
10	131.5	8.9	233	1 S22052	tumor necrosis fac
11	131	8.9	234	1 J01344	tumor necrosis fac
12	130.5	8.8	233	1 S24642	tumor necrosis fac
13	129.5	8.8	235	2 I54490	tumor necrosis fac
14	127.5	8.6	204	1 S24641	lymphotoxin - bovi
15	125.5	8.5	233	1 QWHUN	tumor necrosis fac
16	123.5	8.4	235	1 QWMSN	tumor necrosis fac
17	123.5	8.4	235	2 J00029	tumor necrosis fac
18	122	8.3	205	1 QHUX	lymphotoxin alpha
19	121	8.2	234	1 JH0529	tumor necrosis fac
20	115.5	7.8	193	2 S06192	tumor necrosis fac
21	114	7.7	202	1 B27303	tumor necrosis fac
22	113.5	7.7	185	2 S52715	tumor necrosis fac
23	113.5	7.7	306	2 I49139	lymphotoxin-beta -
24	112.5	7.6	638	1 Q0BY2M	mRNA maturase b14
25	111.5	7.5	202	1 JN0869	tumor necrosis fac
26	109	7.4	652	2 I48083	amphotropic murine
27	107	7.2	197	1 JH0309	tumor necrosis fac
28	102	6.9	244	2 A46066	lymphotoxin beta -
29	100	6.8	865	2 AB1658	probable membrane

30	99.5	6.7	233	2 S11688	tumor necrosis fac
31	97.5	6.6	448	2 P95122	protein kinase, pr
32	95	6.4	345	2 T14707	DNA ligase homolog
33	95	6.4	365	2 T15010	hypothetical prote
34	95	6.4	455	2 G95104	hypothetical prote
35	94.5	6.4	4981	2 T18489	hypothetical prote
36	94	6.4	1465	2 T23056	chromodomain helic
37	92.5	6.3	833	1 A31593	heat shock transcr
38	92.5	6.3	1538	2 T29095	cardiac muscle fac
39	91	6.2	1176	2 JN0583	myosin-light-chain
40	90.5	6.1	502	2 JC2491	serine/threonine k
41	90.5	6.1	502	2 A53444	activin receptor-1
42	90.5	6.1	1284	2 T40578	hypothetical prote
43	90	6.1	907	2 E96636	hypothetical prote
44	89.5	6.1	313	2 T03031	NBS-LRR type resis
45	89	6.0	328	2 B59296	alpha-N-arabinotur

ALIGNMENTS

RESULT 1

A53062  
Fas ligand - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A53062  
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag  
Cell 76, 969-976, 1994  
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in  
A;Reference number: A53062; MUID:94185175; PMID:7511063  
A;Accession: A53062  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-279 <TAK>  
A;Cross-references: UNIPROT:P41047; GB:U06948; MID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 12.8%; Score 189.5; DB 2; Length 279;  
Best Local Similarity 25.8%; Pred. No. 1.7e-08;  
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

Qy	83	QLRQLVRKMLTSTSEETISTVQEKQNIPLVRRGQPVAAHITGTRGRNTLSSPNSK	142
Db	111	ELREFTNQSL-----KVSSFQKIAMPSTFSEKGPSSV-AHUTG-----NPHSR	154
Qy	143	NEKALGRKINSWSSRSRSGHSFLSNLHRLNGELVIHKGFTYIYSQTYFRQEEIKENTKN	202
Db	155	S1PL-----EWEDT-YGTALISGVKYKGGVLINETGLYFVYSKVYFRGQ-----SCN	201
Qy	203	DKQMVQYIY-KYTSYDPDILLMKASR-NSCWSKDAEYGLYSIYOGGIFELKENDRIFVSV	260
Db	202	NQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVENTLSADHLYVNI	259
Qy	261	TNEHLIDMDHEASFGAF	278
Db	260	SQSLINFESKTFFGDLY	277

RESULT 2

I38707  
Fas ligand - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I38707; JC2340; S57565; I38554  
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.  
Int. Immunol. 6, 1567-1574, 1994  
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.  
A;Reference number: I38707; MUID:95127560; PMID:7826947  
A;Accession: I38707  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-281 <RES>  
A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:G595430; PIDN:AAC50124.1; PID:G5954

R;Mita, E.; Hayaashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994  
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
A;Reference number: JC2340; MUID:95071350; PMID:7980502  
A;Accession: JC2340  
A;Molecule type: DNA  
A;Residues: 1-281 <MIT>  
A;Cross-references: GB:D38122; DDBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:gi369902  
R;Schatzlein, C.B.  
A;Reference number: S57565  
A;Accession: S57565  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-281 <SCH>  
A;Cross-references: EMBL:X89102; NID:G887455; PID:G887456  
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G J. Exp. Med. 181, 71-77, 1995  
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.  
A;Reference number: I38554; MUID:95105731; PMID:7528780  
A;Accession: I38554  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-281 <RE2>  
A;Cross-references: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628  
C;Genetic: FasL  
A;Introns: 151/1; 116/3  
A;Keywords: glycoprotein; transmembrane protein  
F;80-102/Domain: transmembrane #status predicted <TM>  
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;  
Best Local Similarity 22.1%; Pred. No. 3 4e-08;  
Matches 63; Conservative 54; Mismatches 82; Indels 86; Gaps 11;

QY 4 MEVGGPSLGQTCLVIFVTLQSLCAV---TYVYFNLKQMDKYKSGIACFLKE 60  
DB 71 LKKRGHSTG-LCLLVWFVVALVGLGLGMFLHLOKELARESTSQMHTASSLEK 129  
QY 61 DSYWPNDEESMNSPCWQVKWQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
DB 130 QIGHPSPPPE-----KKELRV----- 146  
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180  
DB 147 ---AHLT---GKSNRSMP-----LEWDET-YGIVLLSGVYKKGGLVINETG 187  
QY 181 FYIYISQTYFRFOEIKENTKNDKQMVQYIY-KYTSYDPDILLMKARN-----CWSK 233  
DB 188 LYPVSKVYFRGQ-----SCNNLPLSHKVMYRNSKYPODLVVMGKQMSYCTTGQWWAR 241  
QY 234 DAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
DB 242 -----SSYLGAVFNLTSADHLVNVNSELVNFYESOTFFGLY 279

RESULT 3  
A49266  
fas ligand - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A49266  
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.  
Cell 75, 1169-1178, 1993  
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family.  
A;Reference number: A49266; MUID:94084792; PMID:7505205  
A;Accession: A49266  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-278 <SUD>  
A;Cross-references: UNIPROT:P36940; GB:U03470; NID:G440178; PIDN:AACS2129.1; PID:G440179  
C;Keywords: glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;  
Best Local Similarity 27.5%; Pred. No. 1.8e-07;  
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

QY 100 ISTVQEKQONISPLVRERQPVAAHITCT-RGRSNTLSSPNSKNEKALGRKINSWESSR 158  
DB 121 VGSFEKQIANPSTPSETKKPRSV-AHLTGNRSRSLP-----EWEDT- 162  
QY 159 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIY-KYTSYP 217  
DB 163 YGTALISGVYKKGGLVINEAGLYFYVKYFRGQ-----SCNSQPLSHKVMYRNFKYP 216  
QY 218 DPILLMKAR-NSCWSKDAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276  
DB 217 GDLVLMEEKKLVNCTI--CQIWAHSSYLGAVFNLTVDHLYVNISQLSINFEESKTFEG 274  
QY 277 AF 278  
DB 275 LY 276

## RESULT 4

SD3090  
CD40 ligand - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
A;Accession: S53090  
R;Wentens, B.E.L.C.; Muriuki, M.  
submitted to the EMBL Data Library, February 1995  
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.  
A;Reference number: S53090  
A;Accession: S53090  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <MER>  
A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:G732569; PIDN:CAA88363.1; PID:G73255

Query Match 11.1%; Score 164; DB 2; Length 261;  
Best Local Similarity 25.9%; Pred. No. 2.3e-06;  
Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;

QY 6 VGGPSLGTCVLIVFTVLL--QSLCAVAVYVYFNLKQMDKYKSGIACFLKEDDS 63  
DB 13 VATGPPVSMK-IFMYLLTVFLITQIMIGSALFAVYLHRLDKIEDERNLHEDFVFMK--T 68  
QY 64 YNDPNDEESMNS--PCWQVKWQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGQ 121  
DB 69 IORCNKGEGLSLLNCEEIRSRPDLV-KDIMQNK-----VKKEKFNEMHKGQDEPQ- 121  
QY 122 VAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHE 178  
DB 122 IAAHV-----ISEASSKTSVL-----QW--APKGYITLSNNLVLTLENGKQLAVKR 165  
QY 179 KGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDILLMKARNCSWKSQAEY 238  
DB 166 QGFYIYITQVTFCSNRE---TLQAFFIASLCLKSPSGSERILLRAANTHSSSKKPC--G 219  
QY 239 LYSIQGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276  
DB 220 QOSIHLGGVFELOSGASVFVNVTDPQSVSHGTGFTSFG 257

## RESULT 5

I53476  
CD40 ligand - human  
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: S28017; JH0793; S28852; S28694; S28584; S30593  
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; EMO J. 11, 4313-4321, 1992  
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for



A;Reference number: S28017; MUID:93049181; PMID:1385114

A;Accession: S28017

A;Molecule type: mRNA

A;Residues: 1-261 <HOL>

A;Cross-references: UNIPROT:P29965; EMBL:Z15017; NID:G38483; PIDN:CAA78737.1; PID:G38484

R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.

J. Exp. Med. 176, 1543-1550, 1992

A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin

A;Reference number: JH0793; MUID:9304757; PMID:1281209

A;Accession: JH0793

A;Molecule type: mRNA

A;Residues: 1-261 <SPR>

A;Cross-references: GB:X67878; NID:G38411; PIDN:CAA48077.1; PID:G38412

A;Experimental source: peripheral blood T-cell

R;Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.

Eur. J. Immunol. 22, 3191-3194, 1992

A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.

A;Reference number: S26694; MUID:93076854; PMID:1280226

A;Accession: S26694

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-261 <GRA>

A;Cross-references: EMBL:X68550; NID:G37269; PIDN:CAA48554.1; PID:G37270

R;Gauchat, J.P.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.

FEBS Lett. 315, 259-266, 1993

A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e

A;Reference number: S28852; MUID:93138085; PMID:7678552

A;Accession: S28852

A;Molecule type: mRNA

A;Residues: 1-261 <GAU>

A;Cross-references: EMBL:L07414; NID:G180123; PIDN:AAA35662.1; PID:G180124

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln

C;Genetics:

A;Gene: G0B:CD40LG; HIGM1; IMD3

A;Cross-references: GDB:120632; OMIM:308230

A;Map position: Xq26-Xq26

C;Keywords: glycoprotein; transmembrane protein

F;13-44/Domain: transmembrane #status predicted <TM>

F;45-261/Domain: extracellular #status predicted <EXT>

F;6,240/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 10.08; Score 147.5; DB 2; Length 261;

Best Local Similarity 23.78; Pred. No. 5.7e-05;

Matches 66; Conservative 51; Mismatches 99; Indels 63; Gaps 15;

QY 17 VLIVFTVLL--QSLCAVAVYVFTNELKQMDKQKYSKGIACFLKEDDSYNDP-----ND 69

DB 23 IFMYLLTVLITQWISALFAVYLHRLDKIEDERN-----LHEDFVFMKTIQRCNTG 75

QY 70 EESNN-SPCQVQKQLRQKMLRTSETISTVQEKQNIPLVREGRGQVAAHITG 128

DB 76 ERSLSLLNCEIKSQFEGVKDML-NKEET-----KKENSFEWQKGDQNPQ-IAAHV-- 126

QY 129 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVTHEKGFYIY 185

DB 127 -----ISEASKTTSVL-----QW--AEKGYTMSNNLVLTLENGKQLVFKQGLYIY 172

QY 186 SQTYFRFQBEIKENT-----KNDKQMVQYIYKVTSPDPTILLMKASNSCWSKDAEY 237

DB 173 AQVTFCSNRASSQAPFIASLCLKSPGRFER-----ILLRAANTHSAPKPC-- 218

QY 238 GLYSIVQGGIFELKENDRIFSVVTNEHLDMDHAEFPFG 276

DB 219 GQOSIHLGGVFEPLQPGASVFNVTDPFSQVSHGTGFTSFG 257

RESULT 6

A25451

tumor necrosis factor alpha precursor - rabbit

N;Alternate names: cachectin; TNF alpha

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: A25451; J050727

R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayaashi, H.

DNA 5, 149-156, 1986

A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rab

A;Reference number: A25454; MUID:86219711; PMID:3519137

A;Accession: A25454

A;Molecule type: mRNA

A;Residues: 1-234 <ITO>

A;Cross-references: UNIPROT:P04924; GB:M12845; NID:G165759; PIDN:AAA31486.1; PID:G165760

R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.

DNA 5, 157-165, 1986

A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.

A;Reference number: A25451; MUID:86219712; PMID:3519138

A;Accession: A25451

A;Molecule type: DNA

A;Residues: 1-234 <IT2>

A;Note: this sequence differs from that shown in having a Gln inserted between residues

R;Shakhov, A.N.; Kupraev, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.

Gene 95, 215-221, 1990

A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-i

A;Reference number: JH0309; MUID:91065534; PMID:2249779

A;Accession: J050727

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-62, 'Q', 63-234 <SHA>

A;Cross-references: GB:M60340; GB:M35326; NID:G165754; PIDN:AAA31484.1; PID:G165756

C;Genetics:

A;Insertions: 62/3; 80/1; 96/1

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb

F;1-81/Domain: propeptide #status predicted <PRO>

F;82-234/Product: tumor necrosis factor #status predicted <WAT>

F;19,20/Binding site: myristate (lys) (covalent) #status predicted

F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;147-178/Disulfide bonds: #status predicted

Query Match 9.5%; Score 141; DB 1; Length 234;

Best Local Similarity 22.4%; Pred. No. 0.00017;

Matches 62; Conservative 41; Mismatches 98; Indels 76; Gaps 13;

QY 8 GGPGLQGTCLVLIIFTVLQSLCAVAVYVFTNELKQMDKQKYSKGIACFLKEDDSYNDP 67

DB 22 GGPQSKKRCCLSLFSFLD-----VAGATTLF-----CLL--HFRVIGP 58

QY 68 NDESNNSPCWQVQKQLRQLRVKMI-LRTSEETISTVQEKQNIPLVREGRGQVAAHI 126

DB 59 QEESEPN-----LHLVNPVQMVTLRSASRALSD-----KPL-----AHV 94

QY 127 TGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKGFYIYS 186

DB 95 VA-----NPOVEGOL-----QWLSQRANALLANGMKLTDNLQVVPADGLYIYS 138

QY 187 QTYFRFQBEIKENTKNDKQMVQYIYKY-TSYPPDPILLMKASNSCWSKDAEYG-----LY 240

DB 139 QVLFSCQ-----GCRSVLLTHTVSFVSPYKPNKVNLLSAIKSPCHRETEAEAPMAWE 193

QY 241 SIYQGGIFELKENDRIFSVVTNEHLDMDHAEAS-PFG 276

DB 194 PIYLGGVFQLEKGRDLSTEVNQEYLDLAESGVQVYFG 230

RESULT 7

S21738

CD40 ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: S21738

R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.

; Cosman, D.; Spriggs, M.K.

Nature 357, 80-82, 1992

A;Title: Molecular and biological characterization of a murine ligand for CD40.

A;Reference number: S21738; MUID:92244364; PMID:1374165

A;Accession: S21738

A;Molecule type: mRNA



F:19,20/Binding site: myristate (lys) (covalent) #status predicted  
F:82/Binding site: carboxylate (ser) (covalent) #status predicted  
F:146-178/Disulfide bonds: #status predicted

Query Match 8.9%; Score 131; DB 1; Length 234;  
Best Local Similarity 20.8%; Pred. No. 0.0012;  
Matches 60; Conservative 40; Mismatches 89; Indels 100; Gaps 13;

Qy 8 GPGSLGQTCVLIVFTVLQSLCAVYVYVFNELKQMDKYKSGIACFL-----K 59  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 22 GPGSGRRCLCLSLPFL-----VAGATTLF-----CLLHFGVIGPQR 60  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Qy 60 EDDSYNDPDEESMSPCHQVKWLRLVYVFNELKQMDKYKSGIACFL-----K 119  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 61 EEQL-----PNAFQIN-PLAQ-----LSSSRTPS----- 86  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Qy 120 QRVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEK 179  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 87 DKPVAHVVA-----NPAEQGL--QWLSGRANALLANGVKLTQNLVVPILD 130  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Qy 180 GFYIYISQTYRFQEBIKENTKNDKOMQVYIYKYT-----SYDPDILLMKSGNSCSK 233  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 131 GLYLIYSQVLFKQ-----GCPSTHLLTHTISRLAVSYPSKVNLSAISKSPCHTE 181  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Qy 234 DAIEYG-----LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 182 SPQAEAKPWYEPYLGGVFQLEKGPQLSAEINQPNYLDFAESGGVYFG 230  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
RESULT 12  
S24642  
tumor necrosis factor alpha precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: I46047; S24642  
R:Cludde, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.  
Cytokine 5, 336-341, 1993  
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and  
A:Reference number: I46046; MUID:94083525; PMID:8260599  
A:Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798  
A:Accession: I46047  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-233 <CL2>  
A:Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798  
C:Genetics:  
A:Gene: TNFA  
A:Introns: 62/3; 78/1; 94/1  
C:Superfamily: tumor necrosis factor  
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
F:20/Binding site: myristate (lys) (covalent) #status predicted  
F:81/Binding site: carboxylate (ser) (covalent) #status predicted  
F:145-177/Disulfide bonds: #status predicted

Query Match 8.8%; Score 130.5; DB 1; Length 233;  
Best Local Similarity 20.3%; Pred. No. 0.0013;  
Matches 59; Conservative 43; Mismatches 95; Indels 93; Gaps 13;

Qy 3 MMEVQGGPSLGQTCVLIVFTVLQSLCAVYVYVFNELKQMDKYKSGIACFL----- 58  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 17 LSKAGGPGSRCLCLSLPFL-----VAGATTLF-----CLLHFGV 55  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Qy 59 ---KEDDSYNDPDEESMSPCHQVKWLRLVYVFNELKQMDKYKSGIACFL----- 115  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 56 IGQREESPGP-----SINSLVQT-----LSSSQASS----- 85  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Qy 116 ERGPQVAHIITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELV 175  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 86 ---NKPVAHVVA-----DINSPGQL-----WWDSYANALMANGVKLEDNQLV 125  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Qy 176 IHEKGEVYISQTYRFQEBIKENTKNDKOMQVYIYK-----YTSYDPDILLMKSGNSCSK 230  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :  
Db 126 VPADGGLYISQVLPFGQ-----GCPSTHLLTHTISRLAVSYQTKVNLSAISKSPCHRE 180  
||| : : : ||| : : : ||| : : : ||| : : : ||| : : :



A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
A;Experimental source: U-937 cells  
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
Eur. J. Biochem. 235, 431-437, 1996  
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.  
A;Reference number: S62610; MUID:96202967; PMID:86311363  
A;Accession: S62610  
A;Molecule type: protein  
A;Residues: 77-99 <TAK>  
R;D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994  
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter region  
A;Reference number: I54522; MUID:94102809; PMID:7903959  
A;Accession: I54522  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-8 <DAL>  
A;Cross-references: GB:S68530; NID:g544751  
R;Stevenson, P.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
J. Exp. Med. 176, 1053-1062, 1992  
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys  
A;Reference number: A59163; MUID:93018820; PMID:1402651  
A;Contents: annotation; identification of myristylated lysines  
R;Aggarwal, B.B.; Kohr, W.J.; Haas, P.E.; Moffat, B.; Spencer, S.A.; Henszel, W.J.; Brin  
J. Biol. Chem. 260, 2345-2354, 1985  
A;Title: Human tumor necrosis factor. Production, purification, and characterization.  
A;Reference number: A92511; MUID:85130974; PMID:3871770  
A;Contents: annotation; disulfide bond  
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction  
out detriment to normal cells. It can also act synergistically with interferon gamma to  
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely  
ut are produced by different cell types and have different induction kinetics.  
C;Genetics:  
A;Gene: GDB:TNF; TNFA  
A;Cross-references: GDB:120441; OMIM:191160  
A;Map position: 6p21.3-6p21.3  
A;Introns: 62/3; 78/1; 94/1  
C;Complex: homotrimer  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; mac  
F;1-76/Domain: propeptide #status predicted <PRO>  
F;77-233/Product: tumor necrosis factor #status experimental <WAT>  
F;19,20/Binding site: myristate (lys) (covalent) #status experimental  
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental  
F;145-177/Disulfide bonds: #status experimental

	Query Match	8.5%	Score 125.5;	DB 1;	Length 233;
	Best Local Similarity	17.8%	Pred. No. 0.0036;		
	Matches	51;	Conservative	52;	Mismatches 99; Indels 85; Gaps 9;
QY	2	AMMEVGGPSLQTCVLIVFTVLLQSLCVAVTYVYFTNELKOMQDKYSKGIACFLKED	61		
Db	16	ALPKTGGPGGSRCLFLSLFSLIVAGATTLFCLLHFGVIGPQREFFPR-----	65		
QY	62	DSYWDNDSESNPCWQVKNQLRQLVRKMLRTSETISTVQEKQONISPLVRGPOR	121		
Db	66	-----DLSLISPLAQA-----VASSRTPS-----DK	87		
QY	122	VAAHITGTRSRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHKG	181		
Db	88	PVAHVVA-----NQAEQGL--QWLNRRANALLANGVELNDQNLVPSGL	131		
QY	182	YIYSQTYFRFBKEIKENTKNDKQMVQYIYKYT-----SYDPILLMKSAKNSCWSK--	233		
Db	132	YLIYSQVLFKQ-----GCPSTHVLTTHTISRIAVSYQTKVLLSAIKSPCQRETP	182		
QY	234	----DABYGLYSIYQGGIFELKENDRIFSVTNEHLIDMDHEAS-FFG	276		
Db	183	EGAEAKPWEPIYIGGVFQLEKGRLSAEINRPDYLDFAESGVQVFG	229		

Search completed: June 22, 2005, 06:03:12  
Job time : 28.813 secs

Large Blank (uspio)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 115.832 Seconds  
(without alignments)  
1242.266 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGGPSLQGTCLIV.....NEHLIDMDHEASFFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot;\*

2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1	TN10_HUMAN
2	963	65.2	287	2	Q8K3G0
3	930	62.9	291	1	TN10_MOUSE
4	809.5	54.8	304	2	Q7T1F2
5	577.5	39.1	299	2	O6DHG9
6	334.5	22.6	317	2	Q7ZVX9
7	307.5	20.8	287	2	Q90WT9
8	305.5	20.7	214	2	Q9DDZ5
9	291	19.7	63	2	Q6JSD9
10	267.5	18.1	318	1	TN11_RAT
11	258.5	17.5	316	1	TN11_MOUSE
12	251.5	17.0	317	1	TN11_HUMAN
13	189.5	12.8	279	1	TNFC_MOUSE
14	187	12.7	280	1	TNFC_CERTO
15	186	12.6	281	1	TNFC_HUMAN
16	185	12.5	280	1	TNFC_MACFA
17	185	12.5	280	1	TNFC_MACMU
18	185	12.5	280	1	TNFC_MACNE
19	184.5	12.5	279	2	Q7TWT9
20	184	12.4	272	1	TNFS_CHICK
21	182	12.3	282	1	TNFC_PIG
22	180	12.2	282	2	Q8K3Y8
23	178.5	12.1	250	2	Q861W5
24	177.5	12.0	278	1	TNFC_RAT
25	175.5	11.9	169	2	Q9W950
26	175	11.8	252	2	Q80Y20
27	173	11.7	252	2	Q8K3Y7
28	166	11.2	251	2	Q8NFE9
29	164	11.1	261	1	TNFS_BOVIN
30	163.5	11.1	131	2	Q6J3Q6
31	160	10.8	174	1	TN15_HUMAN

32	159.5	10.8	240	1	TN14_HUMAN
33	157	10.6	154	2	Q8MJ19
34	153.5	10.4	227	2	Q7T2Q3
35	152.5	10.3	239	1	TN14_MOUSE
36	152	10.3	261	1	TNFS_CALJA
37	150.5	10.2	261	1	TNFS_AOTTR
38	149.5	10.1	260	1	TNFS_FELCA
39	149	10.1	241	2	Q6U8I7
40	148	10.0	261	1	TNFS_CERTO
41	148	10.0	261	1	TNFS_MACMU
42	147.5	10.0	260	1	TNFS_CANFA
43	147.5	10.0	261	1	TNFS_HUMAN
44	144.5	9.8	216	2	O70332
45	143	9.7	261	1	TNFS_PIG

#### ALIGNMENTS

#### RESULT 1

ID	TN10_HUMAN	STANDARD;	PRT;	281 AA.
AC	P50591;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).			
GN	Names=TNFSF10; Synonyms=APO2L, TRAIL;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;			
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,			
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,			
RA	Goodwin R.G.;			
RT	"Identification and characterization of a new member of the TNF family that induces apoptosis.";			
RL	Immunity 3:673-682(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;			
RA	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,			
RA	Ashkenazi A.;			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family.";			
RL	J. Biol. Chem. 271:12687-12690(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klauser R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci F., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			







DR	HSP; P50591; I2Q.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	InterPro; IPRO06052; TNF family.
DR	InterPro; IPRO08983; TNF_like.
DR	InterPro; IPRO03636; TNF_subf.
DR	Pfam; PF00229; TNF; 1.
DR	PRODom; PD002012; TNF_subf; 1.
DR	SMART; SMO0207; TNF; 1.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS00049; TNF_2; 1.
SQ	SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;
 Query Match 54.8%; Score 809.5; DB 2; Length 304; Best Local Similarity 55.4%; Pred. No. 3.6e-58; Matches 160; Conservative 45; Mismatches 65; Indels 19; Gaps 6;	
Qy	8 GGPSLGQTCLVLIIVTFVLQLSLCAVTVYVPYNELKQMDDKYSGGIACFLKEDSDWDP 67             ::  :   :: :     :: :     :: :     :
Dd	5 GGPSPAHTCGAVLVAVALQSCVAVTVIYFTNELKLMDTYSRGTAAGTGBELGLIQ 64             ::  :   :: :     :: :     :: :     :
Qy	68 N-----DEESNNSPCWQKWOLRLVKMLIRTSEETISTVQ-EKQNISPLVRGPQ- 120 ::  :   :: :     :: :     :: :     :: :     :
Dd	65 NLDVVESKORVADPCWQKVHGLKLIKMMRSRILOENNSAINGTQALGR--RDEPPQG 122 ::  :   :: :     :: :     :: :     :: :     :
Qy	121 --RVAAHITCTGRSNTLTSPNKGKALKRKINSMESSRGHSFSLNLHLRNGELVIH 177 :   :     :: :     :: :     :: :     :: :     :
Dd	123 PTLIAHAHLTGSKRSSA-SPHNYLSYRGIGKHSHWESSRRGHSLFYNNELMNGELVVP 181 :   :     :: :     :: :     :: :     :: :     :
Qy	178 EKFYYIYSQTYFRPQEE-----IKENTKNDKMQVQIYKYTSYPDPIILMKSGARNCSW 231 :   :     :: :     :: :     :: :     :: :     :
Dd	182 QTGFYIYSQTYFRFRENEDDSGLERIKNPQLVQIYKLTNPDPILLMKSAARTSCW 241 :   :     :: :     :: :     :: :     :: :     :
Qy	232 SKDAEYGLYSIQGGIPELKENDIRFVSVTNEHLIDMDHEASFGAFV 280 :   :     :: :     :: :     :: :     :: :     :
Dd	242 SKAEYGLYSYVGGVFQPKREDRIFVSVSNSDIVDMDKAESFFGAFMI 290 :   :     :: :     :: :     :: :     :: :     :
 RESULT 5 Q6DHG9 PRELIMINARY; PRT; 299 AA.  ID Q6DHG9 TISSUE=WHOLE; AC Q6DHG9 SEQUENCE FROM N.A. DT 25-OCT-2004 (TrEMBLrel. 28, Created) DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) DE Zgc:93230. GN Name=zgc:93230; OS Brachydanio rerio (Zebrafish) (Danio rerio). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; OC Cyprinidae; Baniao. OC NCBI_Taxid=7955; FN [1] RP SEQUENCE FROM N.A. RC Tissue=Whole; EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Laussner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S., RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,	

Jones S.J., Marra M.A.;  
"generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
SEQUENCE FROM N.A.  
TISSUE=Whole;  
AC STRAUSBERG R.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBDJ databases.  
DR ENBL; BC076005; AAH76005.1; -  
GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR008983; TNF like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
SQ SEQUENCE 299 AA; 33526 MW; BA76793D2F1ED5 CRC64;

Query Match 39.1%; Score 577.5; DB 2; Length 299;  
Best Local Similarity 42.2%; Pred. No. 3.9e-39;  
Matches 121; Conservative 57; Mismatches 82; Indels 27; Gaps 8

QY 18 LIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKED--DSYWDPNDESMN 74  
DB 15 LLLAALLLQTTIAVATFTTFSNVLSMTKTFSSVSCLMRANLRTIKQGLNGAEGKD 74  
QY 75 SPQVQVQWLRLVRK-MILRTSEETISTVQEEKQNIISPLV-----RERGQQRVAAHITG 128  
DB 75 DPCQVQTQQLHFLIEKSMSSRYQKEITSAVKDEVSRLVPSLVIQDQEDSSRPKIAAHVTG 134  
QY 129 TGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKGFYIYSQT 188  
DB 135 SYTPESEKDGAGLPNRRKYQKIQSWESEK-GLAFLQNLVSLDGLVVPQAGLYIYSQT 193  
QY 189 YER---PQEEIKENTKND-----KQVQYIY-KYTSYDPDPIILLMKSARNSCWSK 233  
DB 194 YFRHTLIEED--ESAREDEYSGMGEVSVRGKPLQYVYKVVSSYQVPIILLMKNARTICWSR 251  
QY 234 DAEGLYSIYQGGIFELKENDRIFSVSTNEHLIDMDHEASFFGAFV 280  
DB 252 DSEGLYSIQAGLFGQLGSGDRFVTYVSNVSTIDMDEKSFPGAFV 298

RESULT 6  
Q7ZYX9 ID Q7ZYX9 PRELIMINARY; PRT; 317 AA.  
AC Q7ZYX9;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Tnfsl01 protein.  
DE Name=tnfsl01;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A8; TISSUE=Whole body;  
RX MEDLINE=24398257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=Whole body;  
 RA Strauberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC044336; AA444336.1; -.  
 DR HSSP; P50591; ID2Q  
 DR ZFIN; ZDB-GENE-010801-1; tnfsf101.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006052; TNF family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF 2; 1.  
 SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;  
 Query Match 22.6%; Score 334.5; DB 2; Length 317;  
 Best Local Similarity 29.2%; Pred. No. 3.7e-19;  
 Matches 83; Conservative 55; Mismatches 113; Indels 33; Gaps 8;  
 QY 18 LIVFTVLLQSLQVAVTVYVFTNELKQMDKQYKSGTACF-----LKEDSYDND-EE 71  
 DB 40 MVVIVVVVLTQIATSTGLFVYLNMSLSQVSGVTEELRLGLNLVGLKQDDI--PEDLAQ 97  
 QY 72 SMNSPCQVQWQLRQVLRK-----ILRTSEETISTVQEKQNIPLVREGRQ 120  
 DB 98 LFGEPCMKLAGIKAYISKVTDTSIISKQTHAARTHTSYNTGSKMTTV-----MQ 150  
 QY 121 RVAAHITGTRGRNT-----LSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 175  
 DB 151 RPSAHLTSSASDNSRPSQDMHQPDHQSCHRPVHTW-ANKSFGAHLNMTLTNGRLR 209  
 QY 176 IHEKGFYIYQYFRP-QBEIKENTKNDKQVYIYKTSYDPDILLMKSAKNSCKD 234  
 DB 210 VPQDGRYLYSQVYFRYFSPSPSDQSSVSHQLVQCIYKTSYLNPIQLLKGVGKTCWAPD 269  
 QY 235 AEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASPFQAF 278  
 DB 270 AEYALHSYQGLFELRAGDEVFVSVSSPTMTWGEDSSSYFGAF 313  
 RESULT 7  
 Q90WT9  
 ID Q90WT9 PRELIMINARY; PRT; 287 AA.  
 AC Q90WT9  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TNF-related apoptosis inducing ligand-like protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bridgham J.T., Johnson A.L.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY057941; AAU23702.1; -.  
 DR HSSP; P50591; ID2Q.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF 2; 1.  
 SQ SEQUENCE 287 AA; 37092 MW; DB06E1C95087B108 CRC64;  
 Query Match 20.8%; Score 307.5; DB 2; Length 287;  
 Best Local Similarity 32.3%; Pred. No. 5.3e-17;  
 Matches 93; Conservative 46; Mismatches 110; Indels 39; Gaps 11;  
 QY 18 LIVFTVLLQ--SLCVAVTVYVFT-----NELKQ--ODKYSKSGIACFLKEDDSYWD 66  
 DB 8 LLHAFSLEQLLPLCTAPEWAGTWSQALQGNAPPRKAGSQSSSELRCLQLINQOEG 67  
 QY 67 PNDEESM-NSPCQVQWQLRQVLRKMLRTSEETI--STVQEKQ---NISP-LVREGRP 119  
 DB 68 SNLEELISQSC---LKLANTIKAVYATVTENVISRVNEAKSYFNISEGQVATKTL 123  
 QY 120 QRVAHI-----TGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLR 170  
 DB 124 GKPSAHLIFRPQNPQPAQDGSRRFGNLS-----QSCRHAITRWEDS-TIHSILQNTYR 175  
 QY 171 NGELVTHEKGFYIYQYFRFOEIKENTKNDKQVYIYKTSYDPDILLMKSAKNSC 230  
 DB 176 DGLRNVNQAGYIYQYFRYSDRGAGARVSPQLVQCINWKTYSQPIQLLKGVGKTC 235  
 QY 231 WSKDARYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASPFQAF 278  
 DB 236 WAPAEYGLHALYQGLFELKAGDELFSVSSLAIDYSDAASVFGAF 283  
 RESULT 8  
 Q9DDZ5  
 ID Q9DDZ5 PRELIMINARY; PRT; 214 AA.  
 AC Q9DDZ5  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TRAIL-like protein.  
 GN Name:tnfsf101;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bobe J., Goetz F.W.;  
 RT "Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish ovary.";  
 RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).  
 DR EMBL; AF250041; AAG47640.1; -.  
 DR HSSP; P50591; ID2Q.  
 DR ZFIN; ZDB-GENE-010801-1; tnfsf101.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006052; TNF family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF 2; 1.  
 SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;



QY 62 -DSYWPNDSESNWSCWQVWQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRBGPQ 120  
 DB 101 QDSTLESETEALPDCRRMKQAFQ-----GAVORELOHIV-----GPQ 139  
 QY 121 R---VAAHITG-----RGRS-----NTLSSPNKNEKALGRKINWESSRSQH 161  
 DB 140 RFGCVPMWEGSWLDVARRGKPAQPAHLTINADIPSGSHKVSU-----SSWYHR-GW 194  
 QY 162 SFLSNLHLRNGELVILHEKGYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYT-SYPDPI 220  
 DB 195 AKISNMTSLNGKLRVQDQGYLYANICFRHHTSGSVPADYQLQVMVYVVKTSIKIPSSH 254  
 QY 221 LMKARSNCWSCDAEYGLYSIQGIFELKENDRIFSVSTNEHLIDMDHEASFFCAFLV 280  
 DB 255 NLMKGGSTKNWCSNGBFHYFVINGVGFKLKLRAGEEISVQVNSPLDPODATYFGAFKV 314

RESULT 11

TN11\_MOUSE STANDARD; PRT; 316 AA.  
 AC O35235; O35306; Q9JJK8; Q9JJK9; Q9RIY0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
 DE induced cytokine) (TRANSE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)  
 DE (OCIF).  
 GN Name=Tnfrsf11; Synonyms=OPGL, RANKL, Trance;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Hybridoma;  
 RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;  
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,  
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
 RA Choi Y.;  
 RA "TRANSE is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells.";  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Thymic lymphoma;  
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;  
 RA Anderson D.N., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
 RA Tometsko M.S., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
 RA Galibert L.;  
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;  
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
 RA Boyle W.J.;  
 RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
 RT differentiation and activation.";  
 RL Cell 93:165-176(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow stroma;  
 RX MEDLINE=98198248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;  
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,  
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto K., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
 RT "Osteoclast differentiation factor is a ligand for  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical  
 RL to TRANCE/RANKL.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=129;  
 RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;  
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,  
 RA Ueda M., Higashio K.;  
 RT "Cloning and characterization of the gene encoding mouse osteoclast  
 RT differentiation factor.";  
 RL Gene 230:121-127(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;  
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;  
 RT "Determination of three isoforms of the receptor activator of nuclear  
 RT factor-kappaB ligand and their differential expression in bone and  
 RT thymus.";  
 RL Endocrinology 142:1419-1426(2001).  
 RN [7]  
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.  
 RX MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;  
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,  
 RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;  
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-  
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family  
 RT member involved in osteoclastogenesis and dendritic cell survival.";  
 RL J. Biol. Chem. 274:13613-13618(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.  
 RX MEDLINE=21464816; PubMed=11581298;  
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;  
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants  
 RT of receptor-ligand specificity.";  
 RL J. Clin. Invest. 108:971-979(2001).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.  
 RX MEDLINE=2139021; PubMed=11733492; DOI=10.1074/jbc.M106525200;  
 RA Ito S., Wakabayashi K., Ubukata O., Hayaishi S., Okada T.;  
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at  
 RT 2.2-A resolution.";  
 RL J. Biol. Chem. 277:6631-6636(2002).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcaemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted  
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O35235-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O35235-2; Sequence=VSP\_006449;  
 CC Name=3;  
 CC IsoId=O35235-3; Sequence=VSP\_006448;  
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,  
 CC but not in nonlymphoid tissues and is abundantly expressed in T  
 CC cells but not in B cells. A high level expression is also seen in  
 CC the trabecular bone and lung.  
 CC -!- PTM: N-glycosylated.  
 CC -!- PTM: The soluble form of isoform 1 derives from the membrane form  
 CC by proteolytic processing. The cleavage may be catalyzed by  
 CC ADAM17. A further shorter soluble form was observed.  
 CC -!- DISEASE: Deficiency in Tnfrsf11 results in failure to form lobulo-

alveolar mammary structures during pregnancy, resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, including the limbs, skull, and vertebrae and have marked chondrodysplasia, with thick, irregular growth plates and a relative increase in hypertrophic chondrocytes.

-1- SIMILARITY: Belongs to the tumor necrosis factor family.

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EMBL; AF013170; AAC71061.1; -  
 EMBL; AF019048; AAB86812.1; -  
 EMBL; AF053713; AAC40113.1; -  
 EMBL; AB008426; BAA25425.1; -  
 EMBL; AB022039; BAA36970.1; -  
 EMBL; AB022036; BAA36970.1; JOINED.  
 EMBL; AB022037; BAA36970.1; JOINED.  
 EMBL; AB022038; BAA36970.1; JOINED.  
 EMBL; AB032771; BAA97257.1; -  
 EMBL; AB032772; BAA97258.1; -  
 EMBL; AB036798; BAA97259.1; -  
 PDB; 1IQ4; X-ray; A/B/C=157-316.  
 PDB; 1J7Z; X-ray; X/Y/Z=146-316.  
 MGD; MGI:1100089; Tnfsl1.  
 GO; GO:0005515; F:protein binding; IPI.  
 GO; GO:0042804; F:protein homooligomerization activity; IDA.  
 GO; GO:0045453; F:bone resorption; IDA.  
 GO; GO:0009887; P:organogenesis; IMP.  
 GO; GO:0001503; P:ossification; IMP.  
 GO; GO:0045670; P:regulation of osteoclast differentiation; IDA.  
 InterPro; IPR006052; TNF family.  
 InterPro; IPR008983; TNF-like.  
 InterPro; IPR003636; TNF\_subf.  
 Pfam; PF00229; TNF; 1.  
 ProDom; PD002012; TNF\_subf; 1.  
 SMART; SM00207; TNF; 1.  
 PROSITE; PS00251; TNF 1; FALSE\_NEG.  
 PROSITE; PS00449; TNF2; 1.  
 3D-structure; Alternative splicing; Cytokine; Differentiation;  
 Direct protein sequencing; Glycoprotein; Receptor; Signal-anchor;  
 Transmembrane.  
 CHAIN 1 316 Tumor necrosis factor ligand superfamily member 11, membrane form.  
 CHAIN 139 316 Tumor necrosis factor ligand superfamily member 11, soluble form.  
 DOMAIN 1 48 Cytoplasmic (Potential).  
 TRANSMEM 49 69 Signal-anchor for type II membrane protein (Potential).  
 DOMAIN 70 316 Extracellular (Potential).  
 SITE 138 139 Cleavage.  
 CARBOHYD 197 197 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 262 262 N-linked (GlcNAc...) (Potential).  
 VARSPLIC 1 117 Missing (in isoform 3).  
 FT VARSPLIC 1 117 /FTid=VSP\_006448.  
 FT VARSPLIC 14 44 SSEEMSGSGVPGVPEGLHPAPSAPAPAPPPA -> TP (in isoform 2).  
 FT VARSPLIC 14 44 /FTid=VSP\_006449.  
 FT VARSPLIC 14 44 G -> D (in Ref. 2).  
 FT VARSPLIC 14 44 Missing (in Ref. 5).  
 CONFLICT 99 99  
 CONFLICT 141 143  
 STRAND 164 169  
 TURN 171 172  
 STRAND 181 182  
 STRAND 186 187  
 TURN 191 192  
 STRAND 194 196  
 STRAND 198 201

FT TURN 202 203  
 Query Match 17.5%; Score 258.5; DB 1; Length 316;  
 Best Local Similarity 26.4%; Pred.No.6.3e-13;  
 Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;  
 QY 10 PSLGTQCLVIVFTVLLQSLCAVAVTVVYFTNKLQKQDKYSGIACF-----LKEDDSY 64  
 Db 43 PAASRMFLALGLGLGQVVCISIALFLYFRAQWD--PNRISDSTHCFYRILRLHENAGL 100  
 QY 65 WDP--NDESMNSPCWQVKQRLVRKMLILTSEETISTVQKQKQNISPL----- 113  
 Db 101 QDSTLESDTLSDSCRRMKQAFQGAQVK-----ELQHVQPFQSGAPAMM 146  
 QY 114 -----VREGPQFVA--AHITGTRGRSNTLSSPNKNEKALGRKINSVESRSSHGSFELS 165  
 Db 147 EGSWLDVAQRGPEAQPFPAHLT-----INAAIPSGSHKVTL-----SSWTHDR-GWAKIS 196  
 QY 166 NLHLRNGELVIEHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYT-SYDPDPIILMK 224  
 Db 197 NMTLSNGKLRVNDGFFYLYANICFRHHETSGVPTDYQLVAVVYVVKTSIKIPSSHNLMK 256  
 QY 225 SARNSCWSKDABYGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 280  
 Db 257 GGSTKNWSGNSEFHFYSINVGGFFKLAGEEISIQVSNPSLLDPDQDQATYFGAFKV 312  
 RESULT 12  
 TN11\_HUMAN STANDARD; PRT; 317 AA.  
 AC 014788; O14723; Q96Q17; Q9P2Q3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).  
 GN Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow, and Peripheral blood;  
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;  
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D., Galibert L.;  
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Lymph node;  
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;  
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Sernaldi G., Guo J., Dalaney J., Boyle W.J.;  
 RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";  
 RL Cell 93:165-176(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RA Ikeda T., Kuroyama H., Hirokawa K.;  
 RL "Determination of human RANKL isoforms.";  
 RN Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 73-317 FROM N.A.  
 RC TISSUE=Thymocytes;





RX MEDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;  
 RA Peitsch M.J., Tschopp J.J.;  
 RT "Comparative molecular modelling of the Fas-ligand and other members  
 of the TNF family.";   
 RL Mol. Immunol. 32:761-772 (1995).  
 RN [3]  
 RN SEQUENCE FROM N.A. (ISOFORM FASL).  
 RX MEDLINE=95196085; PubMed=789405; DOI=10.1016/1074-7613(94)90106-6;  
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
 RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF  
 RT family gene cluster.";   
 RL Immunity 1:131-136 (1994).  
 RN [4]  
 RN SEQUENCE FROM N.A. (ISOFORM FASL).  
 RC STRAIN=BALB/c;  
 RA Fenner M.H., Shioda T., Isselbacher K.J.;  
 RT "Musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two  
 RT amino acids.";   
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RN SEQUENCE FROM N.A. (ISOFORM FASL).  
 RC STRAIN=C3H; TISSUE=Spleen;  
 RX MEDLINE=20021694; PubMed=1052956;  
 RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,  
 RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;  
 RT "Cloning and expression of a short Fas ligand: a new alternatively  
 RT spliced product of the mouse Fas ligand gene.";   
 RL Blood 94:3456-3467 (1999).  
 RN [6]  
 RN CHARACTERIZATION OF VARIANT GLD.  
 RX MEDLINE=96091792; PubMed=7495745;  
 RA Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,  
 RA Rouseau M., Bron C., Renno T., French L., Tschopp J.;  
 RT "Characterization of the non-functional Fas ligand of gld mice.";   
 RL Int. Immunol. 7:1381-1386 (1995).  
 RN [7]  
 RN VARIANTS ALA-184 AND GLY-218.  
 RC STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and  
 RC SLL;  
 RX MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;  
 RA Kiyagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,  
 RA Yagita H.;  
 RT "Polymorphism of murine Fas ligand that affects the biological  
 RT activity."; Acad. Sci. U.S.A. 94:3914-3919 (1997).  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919 (1997).  
 CC -I- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -I- SUBUNIT: Homotrimer (Probable).  
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);  
 CC Secreted (isoforms FASL and FASLS).  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=FasL;  
 CC IsoId=P41047-1; Sequence=Displayed;  
 CC Name=FasLS;  
 CC IsoId=P41047-2; Sequence=VSP\_006445;  
 CC -I- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -I- DISEASE: A deficiency in this protein is the cause of generalized  
 CC lymphoproliferation disease phenotype (gld). Gld mice present  
 CC lymphadenopathy and autoantibody production. The phenotype is  
 CC recessively inherited.  
 CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC  
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 CC -----  
 DR EMBL; U06948; AAA17800.1; -;  
 DR EMBL; U10984; AAA19778.1; -;  
 DR EMBL; S76752; AAB33780.1; -;  
 DR EMBL; U58995; AAB02915.1; -;  
 DR EMBL; AF113335; AAD52106.1; -;  
 DR FIR; AS3062; AS3062.  
 DR HSSP; P50591; LDG6.  
 DR MGD; MGI:99255; Tnfstf6.  
 DR InterPro; IPR008064; Fas ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF0229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS0049; TNF\_2; 1.  
 KW Alternative splicing; Apoptosis; Cytokine; Disease mutation;  
 KW Glycoprotein; Polymorphism; Signal-anchor; Transmembrane.  
 FT CHAIN 1 279  
 FT CHAIN 128 279  
 FT CHAIN 1 78  
 FT TRANSMEM 79 100  
 FT DOMAIN 101 279  
 FT DOMAIN 4 69  
 FT DOMAIN 45 51  
 FT SITE 127 128  
 FT SITE 127 128  
 FT CLEAVAGE (By similarity).  
 FT DISULFID 200 231  
 FT CARBOHYD 117 117  
 FT CARBOHYD 182 182  
 FT CARBOHYD 248 248  
 FT CARBOHYD 258 258  
 FT VARSPLIC 1 210  
 FT VARIANT 184 184  
 FT VARIANT 218 218  
 FT VARIANT 273 273  
 FT SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;  
 SQ  
 Query Match 12.8%; Score 189.5; DB 1; Length 279;  
 Best Local Similarity 25.8%; Pred. No. 2.5e-07;  
 Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;  
 QY 83 QLRQLVRKMLRTSBETISTVQEKQONISPLVRGQFQVAAHITGTRGSRNTLSFNSK 142  
 DB 111 ELREFTNQSL-----KVSSFQKQIANPTPEKPRSV-AHLTG-----NPHSR 154  
 QY 143 NEKALGRKINSWESSRSGHSPLSNLHRLNGELVIHEKGFYYIYSQYFRFQEEIKENTKN 202  
 DB 155 SIPL-----EWEDT-YGTALISGVYKKGGLVINETGLYFVYKVFYRQ-----SCN 201  
 QY 203 DKQMVQYIY-KTYSYDPDILLMKASR-NSCWSKDAEYGLYSIQGIGIFELKENDRIFVSV 260  
 DB 202 NQPLNKHVYRNRSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSAHLYVNI 259  
 QY 261 TNEHLIDMDHEASFFGAF 278  
 DB 260 SLSLINFESKTFGLY 277



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RESULT 14
TNF6 CERTO
ID TNF6_CERTO STANDARD; PRT; 280 AA.
AC Q9BDN1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN Names=TNFSF6; Synonyms=CD95L, FASL;
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT FAS/FasL ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
CC -!- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects (By similarity).
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC -----
CC EMBL: AF344847; AAK37606.1; ..
CC DR HSSP: P50591; 1D2Q
CC DR InterPro: IPR08064; Fas_ligand.
CC DR InterPro: IPR06053; TNF_abc.
CC DR InterPro: IPR06052; TNF_family.
CC DR InterPro: IPR08983; TNF_like.
CC DR InterPro: IPR003636; TNF_subf.
CC DR Pfam: PF00229; TNF_1.
CC DR PRINTS: PR01681; FASLIGAND.
CC DR PRINTS: PR01234; TNFCROSISFCT.
CC DR PRODOM: PD02012; TNF_subf; 1.
CC DR SMART: SM00207; TNF; 1.
CC DR PROSITE: PS00251; TNF_1; 1.
CC DR PROSITE: PS50049; TNF_2; 1.
KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT CHAIN 1 280 Tumor necrosis factor ligand superfamily
FT member 6, membrane form.
FT CHAIN 129 280 Tumor necrosis factor ligand superfamily
FT member 6, soluble form (By similarity).
FT DOMAIN 1 80 Cytoplasmic (Potential).
FT TRANSMEM 81 101 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 102 280 Extracellular (Potential).
FT DOMAIN 4 69 Pro-rich.
FT DOMAIN 45 64 Poly-Pro.
FT SITE 128 129 Cleavage (By similarity).
FT DISULFID 201 232 Potential.

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Query Match 12.7%; Score 187; DB 1; Length 280;
Best Local Similarity 22.1%; Pred. No. 4e-07;
Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;

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Db 70 LKRGHNSTG-LCLLVMPFWLVALVGLGLGMPQLFHLQKELAE-----LRSTS 118
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 64 YNDPNDSESNPCWQVKQLRKLRLTSEETISTVQEKQNIPLVRGPGORVA 123
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 119 -----QKHTASLEKQIGHPSPP-PPKKEQKV 145
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 124 AHITGRGRSNTLSSPNSKNEKALGRKINSWSSRSGHGFSLNHLRNGELVTHEKGFY 183
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 146 AHLTG-----KNSRSMPL-----EWEDT-YGIVLLSGVKYKGGVLINETGLYF 189
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 184 IYSQTYFRFEQRIKENTKNDKQVQYIY-KYTSYDPPIILMKSNRNSKDAEYGLYSI 242
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 190 VYSKVYFRQ-----SCTNLPLSHKVMRNSKYQDLVNMGECKWMS-YCTTGQMAHSS 242
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 243 YQGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 243 YLGAVENTLTDRHLVYVNSELSLVNPFESQTFEGLY 278
   :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 15
TNF6_HUMAN STANDARD; PRT; 281 AA.
AC P48023; Q9BZP9;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN Names=TNFSF6; Synonyms=APTLG1, FASL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
RT lymphocytes.";
RL J. Exp. Med. 181:71-77(1995).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: Gene structure, chromosomal location and species
RT specificity.";
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
SEQUENCE FROM N.A. (ISOFORM 1).
RA Schaeuble C.E., Poehlmann R., Philippson P., Eibel H.;
RN Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayaishi N., Iio S., Takehara T., Hijioaka T., Kasahara A.,
RA Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;

```

RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;  
RT "Isolation and characterization of a new naturally occurring variant of  
RT human Fas ligand that is expressed only in membrane bound form.";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Wilkinson J.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Blood;  
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klugner R.D., Collins F.S., Buetow K.H., Shenmen C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [8]  
RP SEQUENCE OF 1-10 FROM N.A.  
RC TISSUE=Blood;  
RA Matsumura M., Nakanishi Y., Ohba Y.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TVR-218 AND PHE-275.  
RX MEDLINE=97373583; PubMed=9228059; DOI=10.1074/jbc.272.30.18827;  
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,  
RA Tersikh A., Peitsch M.C., Tschopp J.;  
RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";  
RL J. Biol. Chem. 272:18827-18833(1997).  
RN [10]  
RP PROCESSING.  
RX MEDLINE=98087475; PubMed=9427603;  
RA Tanaka M., Itai T., Adachi M., Nagata S.;  
RL Nat. Med. 4:31-36(1998).  
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
CC transduces the apoptotic signal into cells. May be involved in  
CC cytotoxic T cell mediated apoptosis and in T cell development.  
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
CC peripheral tolerance, in the antigen-stimulated suicide of mature  
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3  
CC modulates its effects.  
CC -!- SUBUNIT: Homotrimer (Probable).  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released  
CC into the extracellular fluid, probably by cleavage from the cell  
CC surface.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P48023-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P48023-2; Sequence=VSP\_006443, VSP\_006444;  
CC -!- PTM: N-glycosylated.  
CC -!- PTM: The soluble form derives from the membrane form by  
CC proteolytic processing.  
CC -!- DISEASE: Defects in TNFRSF6 are a cause of autoimmune  
CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as  
CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome

CC involving hemolytic anemia and thrombocytopenia with massive  
CC lymphadenopathy and splenomegaly.  
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2;59-69(2001);  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674\_g.htm".  
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CC -----  
CC EMBL; X89102; CAA61474.1; -  
CC EMBL; U08137; AAC50071.1; -  
CC EMBL; U11821; AAC50144.1; -  
CC EMBL; D38122; BAA07320.1; -  
CC EMBL; AF288573; AAG60017.1; -  
CC EMBL; Z96050; CAB09424.1; -  
CC EMBL; BC017502; AAH17502.1; -  
CC EMBL; AB013303; BAA32542.1; -  
CC EIR; I38707; I38707.  
CC HSSP; P50591; ID20.  
CC Genew; HGNC:11936; TNFRSF6.  
CC H-InVDB; HIX0001337; -  
CC MIM; 134638; -  
CC MIM; 601859; -  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0005102; P:receptor binding; TAS.  
CC GO; GO:0007267; P:cell-cell signaling; TAS.  
CC GO; GO:0006917; P:induction of apoptosis; TAS.  
CC GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IEP.  
CC GO; GO:0007165; P:signal transduction; TAS.  
CC InterPro; IPR008664; Fas\_ligand.  
CC InterPro; IPR006053; TNF\_abc.  
CC InterPro; IPR006052; TNF family.  
CC InterPro; IPR008983; TNF like.  
CC InterPro; IPR003636; TNF\_subf.  
CC Pfam; PF00229; TNF; 1.  
CC PRINTS; PR01681; FASLIGAND.  
CC PRINTS; PR01234; TNECROSISPT.  
CC ProDom; PD002012; TNF\_subf; 1.  
CC PROSITE; PS00251; TNF\_1; 1.  
CC PROSITE; PS50049; TNF\_2; 1.  
CC KW Alternative splicing; Antigen; Apoptosis; Cytokine; Glycoprotein;  
CC KW Signal-anchor; Transmembrane.  
CC CHAIN 1 281  
CC member 6, membrane form.  
CC member 6, soluble form.  
CC member 6, soluble form.  
CC Cytoplasmic (Potential).  
CC Signal-anchor for type II membrane  
CC protein (Potential).  
CC Extracellular (Potential).  
CC Pro-rich.  
CC Poly-Pro.  
CC Cleavage.  
CC Potential.  
CC N-linked (GlcNAc...) (Potential).  
CC N-linked (GlcNAc...) (Potential).  
CC N-linked (GlcNAc...) (Potential).  
CC STSQMHTASSL -> ATPVHLKRS (in isoform  
CC 2).  
CC /FTID=VSP\_006443.  
CC Missing (in isoform 2).  
CC /FTID=VSP\_006444.  
CC P->D,F,R: Lowers binding to TNFRSF6 and  
CC reduces cytotoxicity more than 100-fold.  
CC Y->F,R: Lowers binding to TNFRSF6 and  
CC abolishes cytotoxicity.  
CC F->L: Abolishes binding to TNFRSF6 and  
CC cytotoxicity.



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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 124.948 Seconds  
(without alignments)  
869.796 Million cell updates/sec

Title: US-10-662-429-2  
Perfect score: 1478  
Sequence: 1 MANMEVQGSGSLGQTCVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	2 AAW19777	Aaw19777 Novel cyt
2	1478	100.0	281	2 AAW27134	Aaw27134 Human Apo
3	1478	100.0	281	2 AAW19787	Aaw19787 Human apo
4	1478	100.0	281	2 AAW76829	Aaw76829 Human TL2
5	1478	100.0	281	2 AAW56760	Aaw56760 Human TR
6	1478	100.0	281	2 AAW44354	Aaw44354 Human AGP
7	1478	100.0	281	2 AAW01517	Aaw01517 Protein a
8	1478	100.0	281	2 AAY27012	Aay27012 Human Apo
9	1478	100.0	281	3 AAY81956	Aay81956 Human Apo
10	1478	100.0	281	3 AAB24038	Aab24038 Human PRO
11	1478	100.0	281	3 AAB08545	Aab08545 Amino aci
12	1478	100.0	281	3 AAB28691	Aab28691 Human AGP
13	1478	100.0	281	4 AAB50977	Aab50977 Human PRO
14	1478	100.0	281	4 AAB67243	Aab67243 Human Apo
15	1478	100.0	281	4 AAE11031	Aae11031 Human TNF
16	1478	100.0	281	4 AAB48350	Aab48350 Human TL2
17	1478	100.0	281	5 AAB08133	Aab08133 Human TR
18	1478	100.0	281	5 ABG31630	Abg31630 Human TR
19	1478	100.0	281	5 AAU75062	Aau75062 Human TNF
20	1478	100.0	281	5 AAM51077	Aam51077 Human Apo
21	1478	100.0	281	5 ABP51954	Abp51954 Human Apo
22	1478	100.0	281	5 AAO19095	Aao19095 C neoform
23	1478	100.0	281	5 AAU79593	Aau79593 Human TNF
24	1478	100.0	281	5 ABG73861	Abg73861 Human Apo
25	1478	100.0	281	6 ABU10205	Abu10205 Human Apo

26	1478	100.0	281	6 ABU71443	Abu71443 Human neo
27	1478	100.0	281	6 ABG72738	Abg72738 Human TNF
28	1478	100.0	281	6 AAO29543	Aao29543 Human TR
29	1478	100.0	281	6 ABU08558	Abu08558 Human TNF
30	1478	100.0	281	6 ABR42313	AbR42313 Human TR
31	1478	100.0	281	6 ABG71905	Abg71905 Human TR
32	1478	100.0	281	6 ABP60546	Abp60546 Human tum
33	1478	100.0	281	6 AAE36258	Aae36258 Human TR
34	1478	100.0	281	6 AAO31151	Aao31151 Human TNF
35	1478	100.0	281	6 ABO25125	Abo25125 Human TNF
36	1478	100.0	281	7 ADB61471	Adb61471 Native hu
37	1478	100.0	281	7 ADC35202	Adc35202 Human TNF
38	1478	100.0	281	7 ADD14080	Add14080 Human src
39	1478	100.0	281	7 ADD19010	Add19010 Human dis
40	1478	100.0	281	7 ABW02276	Abw02276 Human TR
41	1478	100.0	281	8 ADE76953	Ade76953 Human pro
42	1478	100.0	281	8 ADK72311	Adk72311 Human Apo
43	1478	100.0	281	8 ADK72303	Adk72303 Human Apo
44	1478	100.0	281	8 ADK72304	Adk72304 Human Apo
45	1478	100.0	281	8 ADK72296	Adk72296 Human wil

ALIGNMENTS

RESULT 1  
AAW19777  
ID :AAW19777 standard; protein; 281 AA.  
XX  
AC AAW19777;  
XX  
DT 22-SEP-1997 (first entry)  
XX  
DE Novel cytokine Apo-2 ligand.  
XX  
KW Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..281  
FT /note= "Claim 4"  
FT Region 1..14  
FT /label= Cytoplasmic\_region  
FT Protein 15..281  
FT /note= "Claim 3"  
FT Region 15..40  
FT /label= Transmembrane\_region  
FT Protein 41..281  
FT /note= "Claim 2"  
FT Region 41..281  
FT /label= Extracellular\_region  
FT Modified-site 109  
FT /label= Glycosylation  
FT Protein 114..281  
FT /note= "putative N-linked glycosylation site"  
FT /note= "Claim 1"  
XX  
WO9725428-A1.  
17-JUL-1997.  
XX  
08-JAN-1997; 97WO-US000272.  
XX  
09-JAN-1996; 96US-00584031.  
XX  
(GSEH ) GENENTECH INC.  
XX  
Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX  
WPI; 1997-372867/34.  
XX  
N-PSDB; AAT72796.

PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce  
 PT apoptosis for the treatment of breast and colon cancer.  
 XX  
 PS Claim 4; Fig 1a; 72pp; English.  
 XX  
 CC A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian  
 CC cell apoptosis. It is believed to be a member of the tumour necrosis  
 CC factor cytokine family. Its amino acid sequence was deduced from a cDNA  
 CC clone (AAT72796) isolated from a human placental cDNA library. Apo-2  
 CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-  
 CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells  
 CC transformed or transfected with a vector contg. Apo-2 ligand nucleic  
 CC acid. They can be used to induce apoptosis in mammals and to treat  
 CC pathological conditions such as cancer (esp. breast or colon cancer) or  
 CC to raise antibodies useful in diagnostic assays  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMVEVGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60  
 DB 1 MAMVEVGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60  
 QY 61 DSDYWDPNDEESNPSQWQVQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 DB 61 DSDYWDPNDEESNPSQWQVQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYPPDPILLMKSARNSCWSDASYGLY 240  
 DB 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYPPDPILLMKSARNSCWSDASYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 RESULT 2  
 AAW27134  
 ID AAW27134 standard; protein; 281 AA.  
 XX  
 AC AAW27134;  
 XX  
 DT 02-APR-1998 (first entry)  
 XX  
 DE Human Apoptosis inducing molecule-I (AIM-I).  
 XX  
 KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;  
 KW tumour necrosis factor ligand superfamily; AIM-I altered expression;  
 KW neoplasia inhibition; anti-inflammatory agent.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9733899-A1.  
 XX  
 PD 18-SEP-1997.  
 XX  
 PF 14-MAR-1996; 96WO-US003773.  
 XX  
 PR 14-MAR-1996; 96WO-US003773.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM;  
 XX  
 DR WPI; 1997-470807/43.  
 DR N-PSDB; AAT85210.

XX  
 PT New isolated apoptosis inducing molecule-I - used to develop products for  
 PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft  
 PT versus host disease or inflammation.  
 XX  
 PS Claim 2; Fig 1; 82pp; English.  
 XX  
 CC The present sequence represents a human Apoptosis inducing molecule-I  
 CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand  
 CC superfamily. The products can be used in the diagnosis and treatment of  
 CC disorders related to under-expression, over-expression or altered  
 CC expression of AIM-I. AIM-I or agonists can be used for treating  
 CC autoimmune disorders including systemic lupus erythematosus,  
 CC immunoproliferative disease lymphadenopathy (IPL),  
 CC angioimmunoproliferative disease lymphadenopathy (AIL), rheumatoid arthritis,  
 CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit  
 CC neoplasia such as tumour cell growth, to treat restenosis, to regulate  
 CC haematopoiesis in endothelial cell development, to stimulate peripheral  
 CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be  
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or  
 CC osteoporosis, for preventing graft-host rejection, and as anti-  
 CC inflammatory agents, for treating endotoxic shock or to prevent  
 CC activation of HIV  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 1478; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMVEVGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60  
 DB 1 MAMVEVGGPSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60  
 QY 61 DSDYWDPNDEESNPSQWQVQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 DB 61 DSDYWDPNDEESNPSQWQVQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYPPDPILLMKSARNSCWSDASYGLY 240  
 DB 181 FYIYSQTYFRFOEEIKENTKNDKQVQYIYKYTSYPPDPILLMKSARNSCWSDASYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 RESULT 3  
 AAW19787  
 ID AAW19787 standard; protein; 281 AA.  
 XX  
 AC AAW19787;  
 XX  
 DT 24-SEP-1997 (first entry)  
 XX  
 DE Human apoptosis inducer cytokine TRAIL.  
 XX  
 KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;  
 KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;  
 KW thrombotic microangioplasty; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Domain 1..18  
 FT Domain /label= Cytoplasmic\_domain  
 FT Domain 19..38  
 FT Domain /label= Transmembrane\_domain  
 FT Domain 39..281

```

FT /label= Extracellular domain
FT /note= "contains a receptor-binding region"
FT 89..90
FT Cleavage-site
FT /note= "potential KEX2 protease processing site"
FT 109..111
FT Modified-site
FT /note= "potential N-glycosylation site"
FT 149..150
FT Cleavage-site
FT /note= "potential KEX2 protease processing site"
FT W09701633-A1.
PN
XX
XX 16-JAN-1997.
XX
XX 25-JUN-1996; 96WO-US010895.
XX
XX 29-JUN-1995; 95US-00496632.
PR
XX 01-NOV-1995; 95US-00548368.
XX
XX (IMMUNEX CORP.
XX
XX WIley SR, Goodwin RG;
XX
XX WPI; 1997-118715/11.
DR
XX N-PSDB; AAT72847.
XX
XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
PT cells - useful for treating thrombotic microangiopathy, cancer and viral
PT infection and for use in assays.
XX
XX Claim 10; Page 43-44; 62pp; English.
XX
XX Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
CC (AAW1978) is a novel cytokine that induces apoptosis of certain target
CC cells, including cancer cells and virally infected cells. Its amino acid
CC sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
CC vector pBC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
CC polypeptides) can be expressed in host cells and used in the treatment of
CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
CC to raise antibodies that may be useful for treating thrombotic
CC microangiopathies
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRRGPQ 120
DB 61 DDSYWDNDDESNMPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRRGPQ 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOBEIKENTKQWQVIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOBEIKENTKQWQVIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
XX
XX RESULT 4
XX AAAT76829
XX ID AAAT76829 standard; protein; 281 AA.
XX AC AAAT76829;

```

```

XX 25-JAN-1999 (first entry)
XX Human TL2 protein.
XX
XX TR6; tumour necrosis factor related receptor; human; treatment; stroke;
XX inflammation; arthritis; septicaemia; autoimmune disease; restenosis;
XX transplant rejection; infection; ischaemia; brain injury; bone disease;
XX acute respiratory disease syndrome; acquired autoimmune disease syndrome;
XX AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
XX TL2. tumour necrosis factor-related apoptosis-inducing ligand.
XX
XX Homo sapiens.
XX
XX EP870827-A2.
XX
XX 14-OCT-1998.
XX
XX 23-DEC-1997; 97EP-00310562.
XX
XX 14-MAR-1997; 97US-0041230P.
XX 09-MAY-1997; 97US-00853684.
XX 22-AUG-1997; 97US-00916625.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Deen KC, Young PR;
XX
XX WPI; 1998-523156/45.
XX N-PSDB; AAV63096.
XX
XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
XX polypeptide, antibody, agonist, antagonist, etc.
XX
XX Disclosure; Page 32-33; 34pp; English.
XX
XX This sequence represents the human tumour necrosis factor (TNF)-related
XX receptor, TL2 (also known as tumour necrosis factor-related apoptosis-
XX inducing ligand, TRAIL). This protein is used in a method resulting in
XX the isolation of the novel human TNF related receptor, TR6. TR6
XX polypeptides and polynucleotides can be used in the treatment of chronic
XX and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g.
XX inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
XX host disease, infection, stroke, ischaemia, acute respiratory disease
XX syndrome, restenosis, brain injury, (acquired autoimmune disease
XX syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
XX disorders), atherosclerosis and Alzheimers disease
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRRGPQ 120
DB 61 DDSYWDNDDESNMPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRRGPQ 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOBEIKENTKQWQVIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOBEIKENTKQWQVIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

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RESULT 5
AAW56760
ID AAW56760 standard; protein; 281 AA.
XX
XX
AC AAW56760;
XX
XX 05-AUG-1998 (first entry)
XX
XX Human TRAIL polypeptide.
XX
XX Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
XX cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 1..18
XX /note= "N-terminal cytoplasmic domain"
XX Region 19..38
XX /note= "transmembrane region"
XX Domain 39..281
XX /note= "extracellular domain"
XX
XX US5763223-A.
XX
XX 09-JUN-1998.
XX
XX 25-JUN-1996; 96US-00670354.
XX
XX 29-JUN-1995; 95US-00496632.
XX
XX 01-NOV-1995; 95US-00548368.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Goodwin RG, Wiley SR;
XX
XX WPI; 1998-347322/30.
XX
XX N-PSDB; AAV29518.
XX
XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
XX for producing recombinant polypeptides for research and therapy of
XX leukaemia, lymphoma, melanoma and viral infections.
XX
XX Claim 1; Col 33-36; 28pp; English.
XX
XX This represents a human tumour necrosis factor related apoptosis ligand
XX (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
XX apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
XX for producing the recombinant TRAIL polypeptides, which may be useful in
XX studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
XX (e.g. to isolate antigens for vaccine development). The polypeptides can
XX be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
XX treatment of blood or bone-marrow), or to treat viral infections
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
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XX
XX 1 MAMVEQGPGSLGQTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
XX
XX 61 DDSYDPNDEESMNSPCWQKWLRLVVKXILRTSEETISTVQEKQNIPLVRERGPQ 120
XX
XX 61 DDSYDPNDEESMNSPCWQKWLRLVVKXILRTSEETISTVQEKQNIPLVRERGPQ 120
XX
XX 121 RVAAHITGTRNTLSSPNKNEKALGRKINSWESSRSGHSLNLHLANGSLVTHEKG 180
XX
XX 121 RVAAHITGTRNTLSSPNKNEKALGRKINSWESSRSGHSLNLHLANGSLVTHEKG 180

```

```

QY 181 FYIYSQTYFRQEIEIKENTKNDKQMVQIYKYTSYDPDPILLMKSNCSWSDAEYGLY 240
DB 181 FYIYSQTYFRQEIEIKENTKNDKQMVQIYKYTSYDPDPILLMKSNCSWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 6
AAW44354
ID AAW44354 standard; protein; 281 AA.
XX
XX AC AAW44354;
XX
XX 28-MAY-1998 (first entry)
XX
XX Human AGP-1.
XX
XX Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
XX bone resorption; haematopoietic disease.
XX
XX Homo sapiens.
XX
XX WO9746686-A2.
XX
XX 11-DEC-1997.
XX
XX 06-JUN-1997; 97WO-US009895.
XX
XX 07-JUN-1996; 96US-00660562.
XX
XX (AMGB-) AMGEN INC.
XX
XX Johnson MJ, Simonet WS, Danilenko DM;
XX WPI; 1998-042194/04.
XX
XX N-PSDB; AAV15295.
XX
XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
XX useful for treating inflammation, bone resorption and haematopoietic
XX diseases.
XX
XX Claim 7; Page 36-37; 54pp; English.
XX
XX The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
XX factor (TNF)-related protein, involved in inflammation, myelopoiesis and
XX bone resorption. It has the same nucleic acid and amino acid (aa)
XX sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
XX in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
XX reagents for detecting AGP-1 expression. Nucleic acid complementary to
XX AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
XX used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
XX erythematosus, psoriasis, scleroderma, infection-related inflammation), or
XX bone resorption diseases (e.g. osteoporosis, osteomyelitis,
XX hypercalcaemia, Paget's disease). AGP-1 can be used to treat
XX haematopoietic diseases associated with reduction in the number of bone
XX marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
XX by disease, injury or exposure to myelosuppressive agents. Host cells,
XX transformed with expression vectors containing AGP-1 DNA, are used to
XX produce recombinant AGP-1
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1478; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-137;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAMVEQGPGSLGQTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
XX
XX 1 MAMVEQGPGSLGQTCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60

```



QY 61 DDSYDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
 DB 61 DDSYDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180  
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 DB 181 FYIYSQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 7

AA01517  
 ID RAY01517 standard; peptide; 281 AA.

AC AAY01517;

DT 27-MAY-1999 (first entry)

XX Protein associated with neurodegenerative and autoimmune diseases.

DE Neurodegenerative disease; autoimmune disease; inflammatory disease;  
 KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;  
 KW surface receptor; TRAIL protein.

OS Homo sapiens.

XX FR2766713-A1.

PN 05-FEB-1999.

PD 04-AUG-1997; 97FR-00010176.

PF 04-AUG-1997; 97FR-00010176.

XX (INMR ) BIO MERIEUX.

PA Rieger F, Belliveau JF, Perron H;

XX WPI; 1999-156177/14.

DR Use of polypeptide derived from TRAIL protein for diagnosis of  
 XX degenerative disease - autoimmunity and inflammation, also useful in  
 PT prevention or treatment, and similar use of corresponding ligand and  
 PT nucleic acid.

PS Claim 2; Page 13; 21pp; French.

XX The specification describes the use a polypeptide corresponding to at  
 CC least the primary sequence of part of the present sequence to produce a  
 CC diagnostic, prophylactic or therapeutic composition useful in cases of  
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can  
 CC be used in treatment of neurodegenerative disease, lupus erythematosus,  
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central  
 CC nervous system cells, antigenic and specifically recognise the surface  
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and  
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an  
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific  
 CC receptors, inhibiting formation of natural complex

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGPSLGQTCVLIVFTVLLQSLCAVTVYFTNELKQMDKYSKSGIACFLKE 60

DB 1 MAMMEVQGPSLGQTCVLIVFTVLLQSLCAVTVYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DDSYDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
 DB 61 DDSYDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180  
 QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 DB 181 FYIYSQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 8

AA027012

ID AAY27012 standard; protein; 281 AA.

AC AAY27012;

DT 24-SEP-1999 (first entry)

XX Human Apo-2 ligand (Apo-2L) polypeptide.

DE Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;  
 KW lupus; immune-mediated glomerular nephritis; human.

XX Homo sapiens.

PN WO9936535-A1.

PD 22-JUL-1999.

PF 15-JAN-1999; 99WO-US001039.

PR 15-JAN-1998; 98US-00007886.

XX 15-APR-1998; 98US-00060533.

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;

DR WPI; 1999-444397/37.

XX N-PSDB; AAX86987.

PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis  
 in mammalian cancer cells.

PS Claim 1; Fig 1A; 86pp; English.

XX This sequence represents a novel human cytokine, designated Apo-2 ligand  
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant  
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer  
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to  
 CC induce apoptosis for pathological conditions characterized by decreased  
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-  
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid  
 CC coding sequence can also be used in quantitative and screening diagnostic  
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases  
 CC associated with increased apoptosis

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DSYWDPNDEESMNSPCQWKQOLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
DB 61 DSYWDPNDEESMNSPCQWKQOLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
QY 181 FYYIYSQTYFRFOEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSDAEYGLY 240  
DB 181 FYYIYSQTYFRFOEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9  
AAY81956  
ID AAY81956 standard; protein; 281 AA.  
XX  
AC AAY81956;  
DT 10-JUL-2000 (first entry)  
DE Human Apo-2 ligand protein sequence.  
XX  
KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;  
KW therapy; apoptosis; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US6046048-A.  
XX  
PD 04-APR-2000.  
XX  
PF 08-JAN-1997; 97US-00780496.  
XX  
PR 09-JAN-1996; 96US-0009755P.  
XX  
PA (GETH ) GENENTECH INC.  
PI Kim KJ, Ashkenazi AJ, Chuntharapai A;  
XX  
DR WPI; 2000-282690/24.  
DR N-PSDB; AAA07425.  
XX  
PT New isolated monoclonal antibodies having antigen specificity for Apo-2  
PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo  
PT -2 ligand serum, and for treating diseases associated with increased  
PT apoptosis.  
XX  
PS Claim 9; Fig 1a; 46pp; English.

XX This sequence is the human Apo-2 ligand protein, which is recognised by  
CC monoclonal antibodies produced by the hybridoma cell lines of the  
CC invention. The hybridoma cell lines are deposited under the American Type  
CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258  
CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic  
CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,  
CC tissues, or serum. The antibodies may also be employed as therapeutics.  
CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand  
CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat  
CC pathological conditions or diseases associated with increased apoptosis.  
CC They are also useful for the affinity purification of Apo-2 ligand from  
CC recombinant cell culture or natural sources. The Apo-2 ligand itself may  
CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells  
XX  
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DSYWDPNDEESMNSPCQWKQOLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
DB 61 DSYWDPNDEESMNSPCQWKQOLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
QY 181 FYYIYSQTYFRFOEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSDAEYGLY 240  
DB 181 FYYIYSQTYFRFOEBIKENTKNDKQMVQYIYKYTSYPDPILLMKSAARNSCWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
RESULT 10  
AAB24038  
ID AAB24038 standard; protein; 281 AA.  
XX  
AC AAB24038;  
DT 25-JAN-2001 (first entry)  
XX  
DE Human PRO1096 protein sequence SEQ ID NO:51.  
XX  
KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
KW identification; tumorigenesis; anticancer; detection.  
XX  
OS Homo sapiens.  
XX  
PN WO2000053750-A1.  
XX  
PD 14-SEP-2000.  
XX  
PF 02-DEC-1999; 99WO-US028551.  
XX  
PR 08-MAR-1999; 99WO-US005028.  
PR 01-SEP-1999; 99WO-US020111.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028634.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;  
XX  
DR WPI; 2000-594320/56.  
DR N-PSDB; AAC58120.  
XX  
PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit  
PT the growth of tumors in mammals, and to identify inhibitors of PRO  
PT polypeptide activity or expression.  
XX  
PS Claim 61; Fig 36; 226pp; English.  
XX  
CC The present invention describes an antibody that binds to a human protein  
CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;  
CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;  
CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer  
CC activity and can be used to diagnose tumours in mammals, by detecting  
CC complex formation when the antibody is contacted with test cells.  
CC Increased expression of genes encoding (I) can also be detected to



PT Fusion protein of AGP-1 protein and an Fc region, used to treat  
XX proliferative disorders, immune disorders, and virally-induced disorders.  
XX Claim 3; Fig 2; 9pp; English.

CC The present sequence is human AGP-1, a type II transmembrane protein.  
CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-  
CC terminal portion of the AGP-1 protein have been produced. The fusion  
CC proteins can be used to induce apoptosis in a tissue, and to treat  
CC proliferative disorders, immune disorders, or virally-induced disorders.  
CC The proliferative disorders include cancers, such as breast, prostate,  
CC lung or colon cancer. The viral infections include hepatitis, and  
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may  
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases  
CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion  
CC proteins have increased biological activity compared to the soluble AGP-1  
CC proteins used in prior art therapies

XX  
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DSYNDPNDDEESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
DB 61 DSYNDPNDDEESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180  
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNCSWSDAEYGLY 240  
DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNCSWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13  
AAB50977  
ID AAB50977 standard; protein; 281 AA.

XX AAB50977;  
XX AC  
XX DT 21-MAR-2001 (first entry)  
XX DE Human PRO1096 protein.  
XX KW Human; PRO; cytostatic; neutropic; neuroprotective; respiratory general;  
XX anti-inflammatory; antiangiogenic; immunosuppressive; immunostimulant;  
XX PRO agonist; cancer; inflammatory disorder; immunological disorder.  
XX OS Homo sapiens.  
XX PN WO200073348-A2.  
XX PD 07-DEC-2000.  
XX PF 30-MAY-2000; 2000WO-US014941.  
XX PR 02-JUN-1999; 99WO-US012252.  
XX PR 22-JUN-1999; 99US-0140650P.  
XX PR 23-JUN-1999; 99US-0141037P.  
XX PR 20-JUL-1999; 99US-0144758P.  
XX PR 01-SEP-1999; 99WO-US020111.  
XX PR 08-SEP-1999; 99WO-US020594.

PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030999.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.

XX (GETH ) GENENTECH INC.

XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
XX Shelton DL, Smith V, Watanabe CK, Wood WI;

XX WPI; 2001-016509/02.  
XX N-PSDB; AAC91579.

XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for  
XX treating various tumors, e.g. breast cancer, and other inflammatory,  
XX angiogenic and immunological disorders.

XX Claim 31; Fig 54; 188pp; English.

XX The present sequence is one of twenty eight novel PRO polypeptides. The  
XX PRO polypeptides and their agonists, including antibodies, peptides, and  
XX small molecule agonists, may be used to treat various tumors, e.g.,  
XX cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
XX cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
XX central nervous system cancer, melanoma or leukaemia. They are also  
XX useful for treating other disorders such as neuronal, glial, astrocytal,  
XX hypothalamic and other glandular, macrophagal, epithelial, stromal and  
XX blastocoealic disorders, and inflammatory, angiogenic and immunological  
XX disorders

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DSYNDPNDDEESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
DB 61 DSYNDPNDDEESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180  
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNCSWSDAEYGLY 240  
DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNCSWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14  
AAB67243  
ID AAB67243 standard; protein; 281 AA.

XX AAB67243;  
 XX 18-APR-2001 (first entry)  
 XX Human Apo2 ligand.  
 XX Human; Apo2 ligand: divalent metal ions; viral infection; cancer.  
 XX Homo sapiens.  
 XX WO200100832-A1.  
 XX 04-JAN-2001.  
 XX 26-JUN-2000; 2000WO-US017579.  
 XX 28-JUN-1999; 99US-0141342P.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;  
 XX O'Connell M, Pai R, Shahrokh Z, Simmons L;  
 XX WPI; 2001-123012/13.  
 XX Use of divalent metal ions for making Apo-2 ligand and in formulations  
 XX containing Apo-2 ligand for increasing yield and stability of ligand  
 XX trimers, useful for therapeutic applications.  
 XX Claim 6; Fig 1; 60pp; English.  
 XX The present invention relates to a formulation comprising Apo-2 ligand  
 XX and divalent metal ions. Apo-2 ligand and the formulation are useful for  
 XX treating cancers and viral infections. Addition of divalent metal ions  
 XX for making Apo-2 ligand and formulations containing Apo-2 ligand results  
 XX in increased yield and stability of Apo-2 ligand trimers  
 XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DDSYWDPNDEESNNSPCWQVKWQLROLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
 DB 61 DDSYWDPNDEESNNSPCWQVKWQLROLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180  
 QY 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 DB 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFSVSTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFSVSTNEHLIDMDHEASFFGAFLVG 281

RESULT 15

AAE11031

ID AAE11031 standard; protein; 281 AA.

XX AC AAE11031;

XX XT 18-DEC-2001 (first entry)

XX

DE Human TNF related apoptosis inducing ligand (TRAIL) protein.  
 XX Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;  
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;  
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;  
 XX melanoma.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Domain 1..18  
 XX FT /label= N\_terminal\_cytoplasmic\_domain  
 XX Region 19..38  
 XX FT /label= Transmembrane\_region  
 XX Domain 39..281  
 XX FT /label= Extracellular\_domain  
 XX US6284236-B1.  
 XX 04-SEP-2001.  
 XX 26-MAY-1999; 99US-00320424.  
 XX 29-JUN-1995; 95US-00496632.  
 XX 01-NOV-1995; 95US-00548368.  
 XX 25-JUN-1996; 96US-00670354.  
 XX 26-MAR-1998; 98US-00048641.  
 XX 10-NOV-1998; 98US-00190046.  
 XX (IMMV ) IMMUNEX CORP.  
 XX Wiley SR, Goodwin RG;  
 XX WPI; 2001-595463/67.  
 XX N-PSDB; AAD18395.  
 XX New tumor necrosis factor related apoptosis inducing ligand polypeptides  
 XX for treating viral infections (e.g. bovine viral diarrhoea or human  
 XX immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).  
 XX Claim 2; Col 45-48; 41pp; English.  
 XX The invention relates to a cytokine designated as tumour necrosis factor  
 XX (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis  
 XX of certain target cells, including cancer cells and virally infected  
 XX cells. The TRAIL polypeptides are useful in killing cancer cells, in  
 XX treating viral infections (e.g. bovine viral diarrhoea or human  
 XX immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and  
 XX melanoma), as a research reagent useful in studying apoptosis including  
 XX the regulation of programmed cell death. TRAIL DNA sequences may be  
 XX employed in developing a gene therapy approach to treating disorders  
 XX mediated by defective or insufficient amounts of TRAIL, in the production  
 XX of TRAIL polypeptides and as probes or primers in polymerase chain  
 XX reactions (PCR). The present sequence is human TRAIL protein  
 XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-137;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DDSYWDPNDEESNNSPCWQVKWQLROLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
 DB 61 DDSYWDPNDEESNNSPCWQVKWQLROLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180

Qy 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

Search completed: June 22, 2005, 06:07:13  
Job time : 128.948 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:01:21 ; Search time 652.628 Seconds  
(without alignments)  
165.329 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

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Scoring table: BLOSUM62

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Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1478	100.0	281	9	US-09-813-329-17
4	1478	100.0	281	9	US-09-193-663-8
5	1478	100.0	281	9	US-09-934-465-1
6	1478	100.0	281	10	US-09-919-039-118
7	1478	100.0	281	13	US-10-011-125-4
8	1478	100.0	281	13	US-10-001-054-54
9	1478	100.0	281	14	US-10-093-766-54
10	1478	100.0	281	14	US-10-174-654-11
11	1478	100.0	281	14	US-10-151-882-41
					Sequence 6, Appli
					Sequence 8, Appli
					Sequence 17, Appl
					Sequence 8, Appli
					Sequence 1, Appli
					Sequence 118, App
					Sequence 4, Appli
					Sequence 54, Appl
					Sequence 54, Appl
					Sequence 11, Appl
					Sequence 41, Appl

12	1478	100.0	281	14	US-10-218-547-20
13	1478	100.0	281	14	US-10-322-673-72
14	1478	100.0	281	14	US-10-139-785-66
15	1478	100.0	281	14	US-10-310-793-26
16	1478	100.0	281	15	US-10-279-687-8
17	1478	100.0	281	15	US-10-292-486-5
18	1478	100.0	281	15	US-10-333-713-1
19	1478	100.0	281	15	US-10-662-429-2
20	1478	100.0	281	15	US-10-202-062-20
21	1478	100.0	281	15	US-10-662-431-2
22	1478	100.0	281	15	US-10-662-430-2
23	1478	100.0	281	15	US-10-652-244-2
24	1478	100.0	281	16	US-10-381-160-5
25	1478	100.0	281	16	US-10-755-889-210
26	1478	100.0	281	16	US-10-491-326-1
27	1478	100.0	281	16	US-10-810-063-2
28	1478	100.0	281	16	US-10-825-282-22
29	1478	100.0	281	16	US-10-825-282-24
30	1478	100.0	281	16	US-10-399-116-5
31	1478	100.0	281	16	US-10-688-845-36
32	1478	100.0	281	16	US-10-861-685-1
33	1478	100.0	281	17	US-10-771-254-1
34	1478	100.0	281	17	US-10-855-559-2
35	1478	100.0	281	17	US-10-451-200-5
36	1478	100.0	281	17	US-10-495-353-1
37	1478	100.0	281	17	US-10-652-973-1
38	1469	99.4	279	13	US-10-066-209-3
39	1456	98.5	279	16	US-10-367-094-22
40	1437	97.2	283	17	US-10-978-203-23
41	1437	97.2	283	17	US-10-738-423-10
42	1287	87.1	266	16	US-10-738-423-10
43	1369.5	85.3	246	9	US-09-855-544A-13
44	1238	83.8	271	16	US-10-781-866-30
45	1017	68.8	208	9	US-09-855-544A-16

#### ALIGNMENTS

RESULT 1.  
US-08-916-625B-6  
; Sequence 6, Application US/08916625B  
; Publication No. US20010010924A1  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH C.  
; APPLICANT: YOUNG, PETER R.  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED  
; TITLE OF INVENTION: RECEPTOR, TR6  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,625B  
; FILING DATE: 22-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/853,684  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: 60/041,230  
; FILING DATE: 14-MARCH-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-50008-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-916-625B-6

Query Match 100.0%; Score 1478; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DDSYDPNDEESNNSPCQVKWQLRQLVRKMLILRTSEETISTVQEKQONISPLVRERGPQ 120  
DB 61 DDSYDPNDEESNNSPCQVKWQLRQLVRKMLILRTSEETISTVQEKQONISPLVRERGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180  
QY 181 FYYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNCSWKDAEYGLY 240  
DB 181 FYYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNCSWKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 2  
US-08-971-317A-8  
Sequence 8, Application US/08971317A  
Publication No. US20010010925A1  
GENERAL INFORMATION:  
APPLICANT: Wiley, Steven R.  
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,317A  
FILING DATE: 17-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goller, Mimi C  
REGISTRATION NUMBER: 39,046  
REFERENCE/DOCKET NUMBER: 6255.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (847) 935-7550

TELEFAX: (847) 938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. US20010010925A1e  
US-08-971-317A-8  
Query Match 100.0%; Score 1478; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DDSYDPNDEESNNSPCQVKWQLRQLVRKMLILRTSEETISTVQEKQONISPLVRERGPQ 120  
DB 61 DDSYDPNDEESNNSPCQVKWQLRQLVRKMLILRTSEETISTVQEKQONISPLVRERGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180  
QY 181 FYYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNCSWKDAEYGLY 240  
DB 181 FYYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNCSWKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 3  
US-09-813-329-17  
Sequence 17, Application US/09813329  
Patent No. US20020012968A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole  
TITLE OF INVENTION: Variants Thereof  
FILE REFERENCE: D0016.jp  
CURRENT APPLICATION NUMBER: US/09/813,329  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: 60/190,816  
PRIOR FILING DATE: 2000-03-21  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 17  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-813-329-17

Query Match 100.0%; Score 1478; DB 9; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DDSYDPNDEESNNSPCQVKWQLRQLVRKMLILRTSEETISTVQEKQONISPLVRERGPQ 120  
DB 61 DDSYDPNDEESNNSPCQVKWQLRQLVRKMLILRTSEETISTVQEKQONISPLVRERGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180



QY 181 FYIYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

## RESULT 4

US-09-193-663-8  
; Sequence 8, Application US/09193663  
; Patent No. US20020055624A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF  
; FILE REFERENCE: 6255, US. 02  
; CURRENT APPLICATION NUMBER: US/09/193,663  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/065,916  
; EARLIER FILING DATE: 1997-11-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYVFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYVFTNELKQMDKYKSGIACFLKE 60  
QY 61 DDSYDPNDEESMNSPCWQVKQLRQLRVKMLRTSEETISTVQEQQNISPLVREGPQ 120  
Db 61 DDSYDPNDEESMNSPCWQVKQLRQLRVKMLRTSEETISTVQEQQNISPLVREGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
QY 181 FYIYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

## RESULT 5

US-09-934-465-1  
; Sequence 1, Application US/09934465  
; Patent No. US20020102233A1  
; GENERAL INFORMATION:  
; APPLICANT: Aehkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669,22US03  
; CURRENT APPLICATION NUMBER: US/09/934,465  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 08/584,031  
; PRIOR FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYVFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYVFTNELKQMDKYKSGIACFLKE 60  
QY 61 DDSYDPNDEESMNSPCWQVKQLRQLRVKMLRTSEETISTVQEQQNISPLVREGPQ 120  
Db 61 DDSYDPNDEESMNSPCWQVKQLRQLRVKMLRTSEETISTVQEQQNISPLVREGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
QY 181 FYIYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

## RESULT 6

US-09-919-039-118  
; Sequence 118, Application US/09919039  
; Publication No. US20030108871A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; FILE REFERENCE: PA-0035 US  
; CURRENT APPLICATION NUMBER: US/09/919,039  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/222,113  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 401  
; SOFTWARE: PERL Program  
; SEQ ID NO 118  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1  
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYVFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYYVFTNELKQMDKYKSGIACFLKE 60  
QY 61 DDSYDPNDEESMNSPCWQVKQLRQLRVKMLRTSEETISTVQEQQNISPLVREGPQ 120  
Db 61 DDSYDPNDEESMNSPCWQVKQLRQLRVKMLRTSEETISTVQEQQNISPLVREGPQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
QY 181 FYIYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
Db 181 FYIYISQTYFRFOEEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281



;; PRIOR APPLICATION NUMBER: 09/709238  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 09/802706  
;; PRIOR FILING DATE: 2001-03-09  
;; PRIOR APPLICATION NUMBER: 09/866034  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 09/872035  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: 09/882636  
;; PRIOR FILING DATE: 2001-06-14  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 09/924419  
;; PRIOR FILING DATE: 2001-08-06  
;; PRIOR APPLICATION NUMBER: 09/927796  
;; PRIOR FILING DATE: 2001-08-06  
;; PRIOR APPLICATION NUMBER: 09/929404  
;; PRIOR FILING DATE: 2001-08-13  
;; PRIOR APPLICATION NUMBER: 09/941992  
;; PRIOR FILING DATE: 2001-08-28  
;; PRIOR APPLICATION NUMBER: 09/946374  
;; PRIOR FILING DATE: 2001-09-04  
;; PRIOR APPLICATION NUMBER: PCT/US98/18824  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: PCT/US99/00106  
;; PRIOR FILING DATE: 1999-01-05  
;; PRIOR APPLICATION NUMBER: PCT/US99/05028  
;; PRIOR FILING DATE: 1999-03-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/08615  
;; PRIOR FILING DATE: 1999-04-20  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: 1999-06-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/20111  
;; PRIOR FILING DATE: 1999-09-01  
;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
;; PRIOR FILING DATE: 1999-09-08  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: 1999-11-30  
;; PRIOR APPLICATION NUMBER: PCT/US99/28551  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/28634  
;; PRIOR FILING DATE: 1999-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: 1999-12-16  
;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/00376  
;; PRIOR FILING DATE: 2000-01-06  
;; PRIOR APPLICATION NUMBER: PCT/US00/03565  
;; PRIOR FILING DATE: 2000-02-11  
;; PRIOR APPLICATION NUMBER: PCT/US00/04341  
;; PRIOR FILING DATE: 2000-02-18  
;; PRIOR APPLICATION NUMBER: PCT/US00/04342  
;; PRIOR FILING DATE: 2000-02-18  
;; PRIOR APPLICATION NUMBER: PCT/US00/05841  
;; PRIOR FILING DATE: 2000-03-02  
;; PRIOR APPLICATION NUMBER: PCT/US00/06884  
;; PRIOR FILING DATE: 2000-03-15  
;; PRIOR APPLICATION NUMBER: PCT/US00/08439  
;; PRIOR FILING DATE: 2000-03-30  
;; PRIOR APPLICATION NUMBER: PCT/US00/13705  
;; PRIOR FILING DATE: 2000-05-17  
;; PRIOR APPLICATION NUMBER: PCT/US00/14042  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: PCT/US00/14941  
;; PRIOR FILING DATE: 2000-05-30  
;; PRIOR APPLICATION NUMBER: PCT/US00/15264  
;; PRIOR FILING DATE: 2000-06-02  
;; PRIOR APPLICATION NUMBER: PCT/US00/22031  
;; PRIOR FILING DATE: 2000-08-11  
;; PRIOR APPLICATION NUMBER: PCT/US00/23522  
;; PRIOR FILING DATE: 2000-08-23  
;; PRIOR APPLICATION NUMBER: PCT/US00/30873

;; PRIOR FILING DATE: 2000-11-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: 2000-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520  
;; PRIOR FILING DATE: 2001-02-28  
;; PRIOR APPLICATION NUMBER: PCT/US01/06666  
;; PRIOR FILING DATE: 2001-03-01  
;; PRIOR APPLICATION NUMBER: PCT/US01/17092  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: PCT/US01/17800  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: PCT/US01/19692  
;; PRIOR FILING DATE: 2001-06-20  
;; PRIOR APPLICATION NUMBER: PCT/US01/21066  
;; PRIOR FILING DATE: 2001-06-29  
;; PRIOR APPLICATION NUMBER: PCT/US01/21735  
;; PRIOR FILING DATE: 2001-07-09  
;; PRIOR APPLICATION NUMBER: PCT/US01/27099  
;; PRIOR FILING DATE: 2001-08-29  
;; NUMBER OF SEQ ID NOS: 91  
;; SEQ ID NO 54  
;; LENGTH: 281  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-001-054-54  
  
Query Match 100.0%; Score 1478; DB 13; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDQKYSKGIACFLKE 60  
|||  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDQKYSKGIACFLKE 60  
|||  
QY 61 DDSYDNDDEESNNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQNTISPLVRERGP 120  
|||  
Db 61 DDSYDNDDEESNNSPCWQVKQLRQLVKRMILRTSEETISTVQEKQNTISPLVRERGP 120  
|||  
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
|||  
Db 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHG 180  
|||  
QY 181 FYYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240  
|||  
Db 181 FYYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWKDAEYGLY 240  
|||  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281  
|||  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281  
|||  
  
RESULT 9  
US-10-093-766-54  
; Sequence 54, Application US/10093766  
; Publication No. US20030013099A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy W.  
; APPLICANT: Jones, David A.  
; APPLICANT: Karpf, Adam R.  
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS  
; FILE REFERENCE: PA-0047 US  
; CURRENT APPLICATION NUMBER: US/10/093,766  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PERL Program  
; SEQ ID NO 54  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1  
US-10-093-766-54

Query Match 100.0%; Score 1478; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSDYDNDPNDDEESMNSPCWQVKWQLRQLVRKMLILRTSEETISTVQEQQNISPLVRERGPO 120  
DB 61 DSDYDNDPNDDEESMNSPCWQVKWQLRQLVRKMLILRTSEETISTVQEQQNISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180

QY 181 FYYIYSQTYFRQOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240  
DB 181 FYYIYSQTYFRQOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 10  
US-10-174-654-11  
; Sequence 11, Application US/10174654  
; Publication No. US20030044937A1  
; GENERAL INFORMATION:  
; APPLICANT: Bienkowski, Michael J  
; Jones, Cynthia J  
; TITLE OF INVENTION: TNF-Related Death Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property  
; Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/174,654  
; FILING DATE: 19-Jun-2002  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerber, Lori L.  
; REGISTRATION NUMBER: 41,113  
; REFERENCE/DOCKET NUMBER: 6111.N CN1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616/833-0974  
; TELEFAX: 616/833-8897  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-174-654-11

Query Match 100.0%; Score 1478; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSDYDNDPNDDEESMNSPCWQVKWQLRQLVRKMLILRTSEETISTVQEQQNISPLVRERGPO 120  
DB 61 DSDYDNDPNDDEESMNSPCWQVKWQLRQLVRKMLILRTSEETISTVQEQQNISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180

QY 181 FYYIYSQTYFRQOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240  
DB 181 FYYIYSQTYFRQOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 11  
US-10-151-882-41  
; Sequence 41, Application US/10151882  
; Publication No. US20030059862A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)  
; FILE REFERENCE: PF554  
; CURRENT APPLICATION NUMBER: US/10/151,882  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293,100  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 41  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-151-882-41

Query Match 100.0%; Score 1478; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSDYDNDPNDDEESMNSPCWQVKWQLRQLVRKMLILRTSEETISTVQEQQNISPLVRERGPO 120  
DB 61 DSDYDNDPNDDEESMNSPCWQVKWQLRQLVRKMLILRTSEETISTVQEQQNISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELVTHEKG 180

QY 181 FYYIYSQTYFRQOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240  
DB 181 FYYIYSQTYFRQOEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 12  
US-10-218-547-20  
; Sequence 20, Application US/10218547  
; Publication No. US20030100074A1  
; GENERAL INFORMATION:

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; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-10-218-547-20

Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNELKQMDKYSKSGIACFLKE 60
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DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNELKQMDKYSKSGIACFLKE 60
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QY 61 DSYWDPNDEESNNSPCWQVKQLRLVRKMLILRTSEETISTVQEKQNIPLVRRGPQ 120
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DB 61 DSYWDPNDEESNNSPCWQVKQLRLVRKMLILRTSEETISTVQEKQNIPLVRRGPQ 120
   |||||

QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
   |||||
DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
   |||||

QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240
   |||||
DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240
   |||||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
   |||||
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
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RESULT 13
US-10-322-673-72
; Sequence 72; Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-322-673-72
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; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-139-785-66

Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNELKQMDKYSKSGIACFLKE 60
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QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 180
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QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240
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DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYPDPILLMKSARNSCWSDAEYGLY 240
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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
   |||||
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
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RESULT 14
US-10-139-785-66
; Sequence 66; Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-139-785-66

Query Match      100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.5e-128;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNELKQMDKYSKSGIACFLKE 60
   |||||
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYYVFTNELKQMDKYSKSGIACFLKE 60
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QY 61 DSYWDPNDEESNNSPCWQVKQLRLVRKMLILRTSEETISTVQEKQNIPLVRRGPQ 120
   |||||
DB 61 DSYWDPNDEESNNSPCWQVKQLRLVRKMLILRTSEETISTVQEKQNIPLVRRGPQ 120
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Qy	121	RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG	180
Db	121	RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG	180
Qy	181	FYYIYSQTVFRQEEIKENTQDKQWQYIYKYTSYDDPILLMKSGARNSCWSKDAEYGLY	240
Db	181	FYYIYSQTVFRQEEIKENTQDKQWQYIYKYTSYDDPILLMKSGARNSCWSKDAEYGLY	240
Qy	241	SIYOGGIFELKENDRIFVSVTNEHLIDMDHASPFGAFLVG	281
Db	241	SIYOGGIFELKENDRIFVSVTNEHLIDMDHASPFGAFLVG	281

Search completed: June 22, 2005, 06:39:13  
Job time : 653.628 secs

RESULT 15  
US-10-310-793-26  
; Sequence 26, Application US/10310793  
; Publication No. US20030198640A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Zhang, Jun  
; APPLICANT: Wei, Ping  
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases  
; FILE REFERENCE: PE573  
; CURRENT APPLICATION NUMBER: US/10/310,793  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: 60/336,695  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 10/226,294  
; PRIOR FILING DATE: 2002-08-23  
; PRIOR APPLICATION NUMBER: 60/314,381  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 09/899,059  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/278,449  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 60/216,879  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 09/559,290  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/180,908  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 60/134,067  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: 60/132,227  
; PRIOR FILING DATE: 1999-05-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: human  
US-10-310-793-26

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Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 32.1756 Seconds  
(without alignments)  
651.935 Million cell updates/sec

Title: US-10-662-429-2  
Perfect score: 1478  
Sequence: 1- MAMMEVQGSPSLGQTCVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1	US-08-670-354-2
2	1478	100.0	281	3	US-08-584-031-1
3	1478	100.0	281	3	US-08-780-496-1
4	1478	100.0	281	3	US-08-883-086-10
5	1478	100.0	281	3	US-09-320-424-2
6	1478	100.0	281	3	US-09-333-593A-6
7	1478	100.0	281	4	US-09-157-864-11
8	1478	100.0	281	4	US-09-825-563-2
9	1478	100.0	281	4	US-09-919-039-118
10	1478	100.0	281	4	US-09-582-450-1
11	1478	100.0	281	4	US-09-934-465-1
12	1478	100.0	281	4	US-10-011-125A-4
13	1478	100.0	281	5	PCT-US96-10895-2
14	1469	99.4	279	3	US-09-072-993C-3
15	1238	83.8	271	4	US-09-569-611C-30
16	988	66.8	253	3	US-09-320-424-11
17	988	66.8	253	4	US-09-825-563-11
18	988	66.8	256	3	US-09-320-424-13
19	988	66.8	256	4	US-09-825-563-13
20	930	62.9	177	3	US-09-105-343A-7
21	930	62.9	291	1	US-08-670-354-6
22	930	62.9	291	3	US-09-320-424-6
23	930	62.9	291	4	US-09-825-563-6
24	930	62.9	291	5	PCT-US96-10895-6
25	850	57.5	161	4	US-09-565-423-7
26	735	49.7	169	4	US-09-569-611C-29
27	654	44.2	183	3	US-09-105-343A-8

28	611	41.3	121	4	US-09-513-999C-7833	Sequence 7833, Ap
29	483	32.7	120	4	US-09-569-611C-32	Sequence 32, Appl
30	482	32.6	101	1	US-08-670-354-4	Sequence 4, Appl
31	482	32.6	101	3	US-09-320-424-4	Sequence 4, Appl
32	482	32.6	101	4	US-09-825-563-4	Sequence 4, Appl
33	482	32.6	101	5	PCT-US96-10895-4	Sequence 4, Appl
34	482	32.6	122	4	US-09-569-611C-31	Sequence 31, Appl
35	446	30.2	85	4	US-09-632-287A-12	Sequence 12, Appl
36	258.5	17.5	294	3	US-08-996-139-11	Sequence 11, Appl
37	258.5	17.5	294	3	US-08-995-659-11	Sequence 11, Appl
38	258.5	17.5	294	3	US-09-215-649A-11	Sequence 11, Appl
39	258.5	17.5	294	4	US-09-577-780-11	Sequence 11, Appl
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42	258.5	17.5	294	4	US-09-871-856-11	Sequence 11, Appl
43	258.5	17.5	294	4	US-09-871-291-11	Sequence 11, Appl
44	258.5	17.5	294	4	US-09-871-650-11	Sequence 11, Appl
45	258.5	17.5	294	4	US-09-865-363-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-08-670-354-2  
; Sequence 2, Application US/08670354  
; Patent No. 5763223  
; GENERAL INFORMATION:  
; APPLICANT: Steven R. Wiley and  
; APPLICANT: Raymond G. Goodwin.  
; TITLE OF INVENTION: Cytokine That Induces Apoptosis  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.5.2  
; SOFTWARE: Microsoft Word, Version 6.0.1  
; CURRENT APPLICATION NUMBER: US/08/670,354  
; FILING DATE: 25-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/496,632  
; FILING DATE: 29-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/548,368  
; FILING DATE: 01-NOV-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2835-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-670-354-2

Query Match 100.0%; Score 1478; DB 1; Length 281;

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Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEQQNISPVLVRERGQ 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584, 031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-584-031-1

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEQQNISPVLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEQQNISPVLVRERGQ 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 3
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim

TITLE OF INVENTION: APO-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-496-1

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSGKIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEQQNISPVLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEQQNISPVLVRERGQ 120
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
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; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134. US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYDNDDESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYDNDDESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180

Qy 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 6
US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-6

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60

Qy 61 DDSYDNDDESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYDNDDESNPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

Qy 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180

Qy 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 5
US-09-320-424-2
; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,369
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QY 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNIPLVRRGPQ 120
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Db 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNIPLVRRGPQ 120
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QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
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Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
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QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPDPILLMKSAARNCSWKDAEYGLY 240
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Db 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPDPILLMKSAARNCSWKDAEYGLY 240
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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 7
US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-11
Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
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QY 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNIPLVRRGPQ 120
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QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPDPILLMKSAARNCSWKDAEYGLY 240
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Db 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPDPILLMKSAARNCSWKDAEYGLY 240
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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 9
US-09-919-039-118
; Sequence 118, Application US/09919039
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Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
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QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPDPILLMKSAARNCSWKDAEYGLY 240
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Db 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPDPILLMKSAARNCSWKDAEYGLY 240
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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 8
US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-825-563-2
Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
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QY 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNIPLVRRGPQ 120
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Db 61 DSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQNIPLVRRGPQ 120
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QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
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Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
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QY 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPDPILLMKSAARNCSWKDAEYGLY 240
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Db 181 FYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPDPILLMKSAARNCSWKDAEYGLY 240
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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 9
US-09-919-039-118
; Sequence 118, Application US/09919039
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Patent No. 6727066  
GENERAL INFORMATION:  
APPLICANT: Kaser, Matthew R.  
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
FILE REFERENCE: PA-0035 US  
CURRENT APPLICATION NUMBER: US/09/919,039  
CURRENT FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: 60/222,113  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 401  
SOFTWARE: PERL Program  
SEQ ID NO 118  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6727066 059509CD1  
US-09-919-039-118

Query Match 100.0%; Score 1478; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
DB 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
QY 181 FYIYSQTYFRFOEEIKENTKDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
DB 181 FYIYSQTYFRFOEEIKENTKDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

## RESULT 10

US-09-582-450-1  
Sequence 1, Application US/09582450  
Patent No. 6740739  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Kelley, Robert P.  
APPLICANT: O'Connell, Mark P.  
APPLICANT: Pitti, Robert M.  
APPLICANT: Schwall, Ralph H.  
TITLE OF INVENTION: Apo-2 Ligand  
FILE REFERENCE: P0978P4  
CURRENT APPLICATION NUMBER: US/09/582,450  
CURRENT FILING DATE: 2001-05-14  
PRIOR APPLICATION NUMBER: US 09/007,886  
PRIOR FILING DATE: 1998-01-15  
PRIOR APPLICATION NUMBER: US 09/060,533  
PRIOR FILING DATE: 1998-04-15  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO 1  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-582-450-1

Query Match 100.0%; Score 1478; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
DB 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
QY 181 FYIYSQTYFRFOEEIKENTKDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
DB 181 FYIYSQTYFRFOEEIKENTKDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

## RESULT 11

US-09-934-465-1  
Sequence 1, Application US/09934465  
Patent No. 6746668  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
TITLE OF INVENTION: Apo-2 Ligand  
FILE REFERENCE: 11669.22US03  
CURRENT APPLICATION NUMBER: US/09/934,465  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 08/584,031  
PRIOR FILING DATE: 1996-01-09  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-934-465-1

Query Match 100.0%; Score 1478; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 3.5e-149;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYYVFTNELKQMDKYSKSGIACFLKE 60  
QY 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
DB 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180  
QY 181 FYIYSQTYFRFOEEIKENTKDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
DB 181 FYIYSQTYFRFOEEIKENTKDKQWQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

## RESULT 12

US-10-011-125A-4  
Sequence 4, Application US/10011125A  
Patent No. 6828121  
GENERAL INFORMATION:  
APPLICANT: Chen, Christina Yu-Ching

```
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US96-10895-2
; US-10-011-125A-4

Query Match      100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB      61 DDSYDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY      121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB      121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
DB      181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10895-2

Query Match      100.0%; Score 1478; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.5e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB      1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY      61 DDSYDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB      61 DDSYDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120

QY      121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB      121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY      181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
DB      181 FYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240

QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-072-993C-3

Query Match      99.4%; Score 1469; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKED 62
DB      1 MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKED 60

QY      63 SYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 122
```

Db 61 SYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQRV 120  
Qy 123 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKGFY 182  
Db 121 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKGFY 180  
Qy 183 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYTPDPILLMKSARNSCWSDAEYGLYSI 242  
Db 181 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYTPDPILLMKSARNSCWSDAEYGLYSI 240  
Qy 243 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

## RESULT 15

US-09-569-611C-30  
; Sequence 30, Application US/09569611C  
; Patent No. 6720182  
; GENERAL INFORMATION:  
; APPLICANT: SAVITZKI et al.  
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS  
; FILE REFERENCE: 2786-0151P  
; CURRENT APPLICATION NUMBER: US/09/569,611C  
; CURRENT FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-569-611C-30.

Query Match 83.8%; Score 1238; DB 4; Length 271;  
Best Local Similarity 85.4%; Pred. No. 1.3e-123;  
Matches 240; Conservative 2; Mismatches 5; Indels 34; Gaps 2;

Qy 1 MAMMEVQGGPSLQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
Db 25 MAMMEVQGGPSLQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 84  
Qy 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
Db 85 DSYWDPNDEESMNSPCWQVKQLRQLVRK-----KSNKIFLPLVRERGPQ 130  
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKG 180  
Db 131 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVIHEKG 190  
Qy 181 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYTPDPILLMKSARNSCWSDAEYGLY 240  
Db 191 FYIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYTPDPILLMKSARNSCWSDAEYGLY 250  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 251 SIYQG-----IDMDHEASFFGAFLVG 271

Search completed: June 22, 2005, 06:02:15  
Job time : 33.1756 secs

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GenCore version 5.1.6  
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QM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 23.187 Seconds  
(without alignments)  
1008.352 Million cell updates/sec

Title: US-10-662-429-2\_COPY\_39\_281

Perfect score: 1287

Sequence: 1 TWELKQMDKYKSGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*\*

2: PIR2:\*\*

3: PIR3:\*\*

4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189.5	14.7	279	2 A53062	Fas ligand - mouse
2	182.5	14.2	281	2 I38707	Fas ligand - human
3	177.5	13.8	278	2 A49266	Fas ligand - rat
4	152	11.8	261	2 S53090	CD40 ligand - bovi
5	138.5	10.8	280	2 S21738	CD40 ligand - mous
6	137	10.6	261	2 I53476	CD40 ligand - huma
7	134.5	10.5	204	1 S17289	tumor necrosis fac
8	131.5	10.2	234	1 A25451	tumor necrosis fac
9	130	10.1	232	1 S12606	tumor necrosis fac
10	129.5	10.1	235	2 I54490	tumor necrosis fac
11	127.5	9.9	204	1 S24641	lymphotoxin - bovi
12	126	9.8	234	1 JQ1344	tumor necrosis fac
13	123	9.6	233	1 QMHUN	tumor necrosis fac
14	122	9.5	205	1 QMHUX	lymphotoxin alpha
15	121	9.4	235	1 QWMSN	tumor necrosis fac
16	121	9.4	235	2 J00029	tumor necrosis fac
17	120	9.3	233	1 S22052	tumor necrosis fac
18	117.5	9.1	234	1 JH0529	tumor necrosis fac
19	115.5	9.0	193	2 S06192	tumor necrosis fac
20	114	8.9	202	1 B27303	tumor necrosis fac
21	113.5	8.8	185	2 S52715	tumor necrosis fac
22	113	8.8	233	1 S24642	tumor necrosis fac
23	111.5	8.7	202	1 JN0869	tumor necrosis fac
24	108.5	8.4	306	2 I49139	lymphotoxin-beta -
25	107	8.3	197	1 JH0309	tumor necrosis fac
26	105	8.2	638	1 QOBV2M	mRNA maturease b14
27	102.5	8.0	652	2 I48083	amphotropic murine
28	102	7.9	244	2 A46066	lymphotoxin beta -
29	98.5	7.7	233	2 S11688	tumor necrosis fac

30	97.5	7.6	448	2 F95122	protein kinase, pr
31	95	7.4	455	2 G95104	hypothetical prote
32	93	7.2	1465	2 T23056	chromodomain helic
33	92.5	7.2	833	1 A31593	heat shock transcr
34	92.5	7.2	1538	2 T29095	cardiac muscle fac
35	92	7.1	865	2 AB1658	probable membrane
36	91	7.1	345	2 T14707	DNA ligase homolog
37	91	7.1	365	2 T15010	hypothetical prote
38	91	7.1	1176	2 JN0583	myosin-light-chain
39	89.5	7.0	313	2 T03031	NBS-LRR type reisi
40	89	6.9	328	2 B59296	alpha-N-arabinofur
41	89	6.9	2278	1 S56274	FAB1 protein - yea
42	88.5	6.9	611	2 S56278	DNA-directed DNA p
43	88.5	6.9	1425	2 E89303	protein C47E8.8 [i
44	88.5	6.9	1675	2 T31473	hypothetical prote
45	88	6.8	826	2 JCS153	mitogen-activated

ALIGNMENTS

RESULT 1

A53062

Fas ligand - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

R/Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag

Cell 76, 969-976, 1994

A/Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in

A/Reference number: A53062; MUID:94185175; PMID:7511063

A/Accession: A53062

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-279 <TAK>

A/Cross-references: UNIPROT:P41047; GB:U06948; NID:G473564; PIDN:AAA17800.1; PID:G473565

Query Match 14.7%; Score 189.5; DB 2; Length 279;

Best Local Similarity 25.8%; Pred. No. 1.2e-08;

Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

Qy	45	QLRQLVRKMLRTSEETISTVQEQQNISPLVRERGPORVAAHITGFRGRSNTLSSPSNK	104
Db	111	ELREFNTQSL-----KVSSEFKQIANPSPSEKKEPRSV-AHLTG-----NPHSR	154
Qy	105	NEKALGRKINSWSSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTXN	164
Db	155	S IPL-----EWEDT-YGTALISGVKKYKGLVINETGLYFVYSKYVFRGQ-----SCN	201
Qy	165	DKQMVOYIY-KYTSYDDPILLMKASR-NSCWSKDAEYGLYSIYQGIGIFELKENDRIPVSV	222
Db	202	NQPLNHKVMYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTADHLYVNI	259
Qy	223	TNEHLIDMDHEASFGCAF	240
Db	260	SQSLINFESEKTFFGLY	277

RESULT 2

I38707

Fas ligand - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004

R/Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A/Title: Human Fas ligand: gene structure, chromosomal location and species specificity.

A/Reference number: I38707; MUID:95127560; PMID:7826947

A/Accession: I38707

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-281 <RES>

A/Cross-references: UNIPROT:P48023; EMBL:U11821; NID:G595430; PIDN:AAC50124.1; PID:G5954

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994  
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
A;Reference number: JC2340; MUID:95071350; PMID:7980502  
A;Accession: JC2340  
A;Molecule type: DNA  
A;Residues: 1-281 <MT>  
A;Cross-references: GB:D38122; DDBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:gl369902  
R;Schatzlein, C.E.  
A;Reference number: S57565  
A;Accession: S57565  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-281 <SCH>  
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G. J. Exp. Med. 181, 71-77, 1995  
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.  
A;Reference number: I38554; MUID:95105731; PMID:7528780  
A;Accession: I38554  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-281 <RE2>  
A;Cross-references: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628  
C;Genetic: FasL  
A;Introns: 151/1; 116/3  
A;Keywords: glycoprotein; transmembrane protein  
F;80-102/Domain: transmembrane #status predicted <TMM>  
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 182.5; DB 2; Length 281;  
Best Local Similarity 27.4%; Pred. No. 4.8e-08;  
Matches 57; Conservative 40; Mismatches 70; Indels 41; Gaps 10;

Qy 44 WQLRQLVRKMI-LRTSEETISTVQEKQNI---SPLVRERGPRQVAAHITGTRGRSNTLS 99  
Db 102 FQLFLQKELAEURESTSQMHTASSLEKQIGHPSP-PPEKKELRKVAHLT--GKSNRS 157  
Qy 100 SPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKGFYIYQTYRFRQEEIK 159  
Db 158 MP-----LEWEDT-YGIVLLSGVKKYKGLVINETGLYFYVKVYFRGQ---- 200  
Qy 160 ENTNDKQMVQYIY-KYTSYPPDILLMKASARN-----CWSKDAEYGLYSYQGGIFEL 212  
Db 201 --SCNLPISHKVYMRNSKYQDLVMEGKMSYCTTGQWAR-----SSVLGAVFNL 251  
Qy 213 KENDRIFSVTNEHLIDMDHEASFFGAP 240  
Db 252 TSADHLVNVVSELSLVNFESQTFGLY 279

RESULT 3  
A49266  
fas ligand - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A49266  
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.  
Cell 75, 1169-1178, 1993  
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family.  
A;Reference number: A49266; MUID:94084792; PMID:7505205  
A;Accession: A49266  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-278 <SUD>  
A;Cross-references: UNIPROT:P36940; GB:U03470; NID:G440178; PIDN:AAC52129.1; PID:g440179  
C;Keywords: glycoprotein; transmembrane protein

Query Match 13.8%; Score 177.5; DB 2; Length 278;  
Best Local Similarity 27.5%; Pred. No. 1.3e-07;  
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

Qy 62 ISTVQEKQNI-SPLVRERGPRQVAAHITGTRGRSNTLS-SPNSKNEKALGRKINSWESSR 120  
Db 121 VSSFQKQIANPSTPSETKKPRSV-AHLTGNPSRSIPL-----EWEDT- 162  
Qy 121 SGHSFLSNLHLRNGELVHEKGFYIYQTYRFRQEEIKENTKNDKQMVQYIY-KYTSYP 179  
Db 163 YGTALISYKVKYKGLVINAEAGLYFYVKVYFRGQ-----SCNSQPLSHKVMYMRNFKYP 216  
Qy 180 DPILLMKASAR-NSCWSKDAEYGLYSYQGGIFELKENDRIFSVTNEHLIDMDHEASFFG 238  
Db 217 GOLVLMEEKKUNYCTT--GQIWAHSSYLGAVENTLVADHLVYNISQSLINFEESKTFPG 274  
Qy 239 AF 240  
Db 275 LY 276

RESULT 4  
S53090  
CD40 ligand - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: S53090  
R;Mertens, B.E.L.C.; Muriuki, M.  
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.  
A;Reference number: S53090  
A;Accession: S53090  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <MER>  
A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:G732569; PIDN:CAA88363.1; PID:g73257

Query Match 11.8%; Score 152; DB 2; Length 261;  
Best Local Similarity 27.1%; Pred. No. 1.7e-05;  
Matches 55; Conservative 39; Mismatches 77; Indels 32; Gaps 10;

Qy 39 CMQVKWQLRQLVRKMI-LRTSEETISTVQEKQNI-SPLVRERGPRQVAAHITGTRGRSNTL 98  
Db 84 CHEIRSRRPEDLV-KOIMQNK-----VKKCKENFEMHKGQDEPQ-IAAHV-----I 127  
Qy 99 SPNSKNEKALGRKINSWESSRSGHSLN--LHLRNG-ELVHEKGFYIYQTYRFRQ 155  
Db 128 SEASSKTTISVL-----QW--APKGYTLLSNLVTLENGKQLAVKRGQFYIYQTYRFRQ 180  
Qy 156 EIKENTKNDKQMVQYIYKYTSYPPDILLMKASARNCSWSKDAEYGLYSYQGGIFELKEN 215  
Db 181 RE-----TLGQAPFIASCLKSPSGSERILLRAANTHSSKPC--GQOSIHLGSGVFELQSG 234  
Qy 216 DRIFSVTNEHLIDMDHEASFFG 238  
Db 235 ASVFNVTDPQSQVSHGTGTFSG 257

RESULT 5  
S21738  
CD40 ligand - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: S21738  
R;Armstrong, R.J.; Fanslow, W.C.; Stockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B.N.  
Nature 357, 80-82, 1992  
A;Title: Molecular and biological characterization of a murine ligand for CD40.  
A;Reference number: S21738; MUID:92244364; PMID:1374165  
A;Accession: S21738  
A;Molecule type: mRNA  
A;Residues: 1-260 <ARM>  
A;Cross-references: UNIPROT:P27548; EMBL:X65453; NID:G50351; PIDN:CAA46448.1; PID:g50352  
C;Keywords: glycoprotein; transmembrane protein  
F;23-46/Domain: transmembrane #status predicted <TMM>  
F;47-260/Domain: extracellular #status predicted <EXT>



F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.8%; Score 138.5; DB 2; Length 260;  
Best Local Similarity 25.1%; Pred. No. 0.00024;  
Matches 47; Conservative 37; Mismatches 72; Indels 31; Gaps 8;  
QY 39 CMQVKKQLRQLVRKMLIRTSEETISTVQEKQKQNIPLVRRGQPVAAAHITGTRGSRNTL 98  
DB 84 CEMRRQFEDLVKIDITLTK-----EEKKENSFEMQKQDQNPQ-IAAHV-----V 126  
QY 99 SSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-ELVIEHKGFIYYSQTYFRFOE 156  
DB 127 SEANSNAASVL-----QM-AKGYITMKNLVMLENGKQLTVKREGLYVYVYQVTFCSNR 180  
QY 157 EIKENTKNDKQMVQYIYKTSYPPDPILLMKSARNSCKDAEYGLYSIYOGGIFELKEND 216  
DB 181 E-----PSSQRPFTVGLWMLKPSIGSERILLKAAANTHSSQLCEQ--QSVHLGGVFELQAGA 234  
QY 217 RIFVSVT 223  
DB 235 SVFVNVT 241

## RESULT 6

I53476  
CD40 ligand - human  
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004  
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593  
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.B.; Chalupny, N.J.; Braesch-Andersen, S.;  
EMBO J. 11, 4313-4321, 1992  
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for  
A;Reference number: S28017; MUID:93049181; PMID:1385114  
A;Accession: S28017  
A;Molecule type: mRNA  
A;Residues: 1-261 <HOL>  
A;Cross-references: UNIPROT:P29965; EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484  
R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.  
J. Exp. Med. 176, 1543-1550, 1992  
A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin  
A;Reference number: JH0793; MUID:93094757; PMID:1281209  
A;Accession: JH0793  
A;Molecule type: mRNA  
A;Residues: 1-261 <SPR>  
A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA8077.1; PID:g38412  
A;Experimental source: peripheral blood T-cell  
R;Graf, D.; Korthauer U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.  
Eur. J. Immunol. 22, 3191-3194, 1992  
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.  
A;Reference number: S26694; MUID:93076854; PMID:1280226  
A;Accession: S26694  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <GRA>  
A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270  
R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.  
FEBS Lett. 315, 259-266, 1993  
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e  
A;Reference number: S28852; MUID:93138085; PMID:7678552  
A;Accession: S28852  
A;Molecule type: mRNA  
A;Residues: 1-261 <GAU>  
A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124  
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln  
C;Genetics:  
A;Gene: GDB:CD40LG; HIGM1; IMD3  
A;Cross-references: GDB:I120632; OMIM:308230  
A;Map position: Xq26-Xq26  
C;Keywords: glycoprotein; transmembrane protein  
F;13-44/Domain: transmembrane #status predicted <TMM>  
F;45-261/Domain: extracellular #status predicted <EXT>.  
F;6,22/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.6%; Score 137; DB 2; Length 261;  
Best Local Similarity 24.6%; Pred. No. 0.00033;  
Matches 52; Conservative 38; Mismatches 73; Indels 48; Gaps 11;  
QY 39 CMQVKKQLRQLVRKMLIRTSEETISTVQEKQKQNIPLVRRGQPVAAAHITGTRGSRNTL 98  
DB 84 CBEIKSQFGFVKDIDL-NKEET-----KKENSFEMQKQDQNPQ-IAAHV-----I 127  
QY 99 SSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-ELVIEHKGFIYYSQTYFRFOE 155  
DB 128 SEASSKTSVL-----QM-AKGYITMKNLVMLENGKQLTVKROGLYIYIAQVTFCSN 180  
QY 156 EIKENT-----KNDKQMVQYIYKTSYPPDPILLMKSARNSCKDAEYGLYSIYOG 207  
DB 181 REASSQAPFIASCLKSPGRFER-----ILLRAANTHSSAKPC--GQOSIHLG 226  
QY 208 GIFELKENDRIFVSVTNEHLIDMDHEASPEF 238  
DB 227 GVFEQPGASVFNVTDPQVSHGTGTSFG 257

## RESULT 7

S17289  
tumor necrosis factor beta precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004  
C;Accession: S17289  
R;Kuhnert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.  
Gene 102, 171-178, 1991  
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal  
A;Reference number: S17289; MUID:91340150; PMID:1874444  
A;Accession: S17289  
A;Molecule type: DNA  
A;Residues: 1-204 <KUH>  
A;Cross-references: UNIPROT:P26445; EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133  
C;Genetics:  
A;Introns: 32/3; 68/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>  
Query Match 10.5%; Score 134.5; DB 1; Length 204;  
Best Local Similarity 24.7%; Pred. No. 0.00039;  
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;  
QY 63 STVQEKQKQNIPLVRRGQPVAAAHITG-----TRGSRNTLSSPNSKNEKALGRKINS 115  
DB 42 SAAQPAHQH-PPKHLARGTLKPAAHLVGDPSTPDSLRWRANT-----DRAPLR---- 88  
QY 116 WESSRSGHSFLSNLHRLNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQMVQYIYKY 175  
DB 89 -----HGFL-----LSNNSLLVPTSGLYFVYQVVFSGEGCFPKATPTPLYLAHEVQLF 137  
QY 176 TS-YPPDPILLMKSARNSCKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEA 234  
DB 138 SSOYPPHVPILLSAQKSCVCPQGPW-VRSVYQGAVELLTQGDQLSTHTDTPHLLSPSS 196  
QY 235 SPFGAF 240  
DB 197 VFFGAF 202  
RESULT 8  
A25451  
tumor necrosis factor alpha precursor - rabbit  
N;Alternate names: cachectin; TNF alpha  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004  
C;Accession: A25454; A25451; J50727  
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.  
DNA 5, 149-156, 1986



Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

QY 72 ISPLVVRGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE-----SRSRGH 123  
Db 56 IGPQREKFPNNLP--IGSMAQTLTLRSSSSQSDKPFVAHVAVNHQVDRQLEWLSRGAN 113

QY 124 SPLSN-LHLRNGELVTHEKGFYIYSQTYFRFOEIKENTKDKQMVOYIYKY-TSPDP 181  
Db 114 ALLANGMDLKNQVLVPADGLYIVSOVLFGQ-----GCSSVLLTHTVSRFAVSYEDK 168

QY 182 ILLMKARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFSVSTNEHLIDMDHEAS 235  
Db 169 VNLLSAIKSPC-PKETPEGSELKPWEPIYLGGVFQLEKGRDLSAEVNLPKYLDFAESGQ 227

QY 236 -FFG 238  
Db 228 VFPG 231

RESULT 11  
S24641  
lymphotoxin - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: I46046; S24641  
R:Cluades, I.; Clueter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.  
Cytokine 5, 336-341, 1993  
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu  
A:Reference number: I46046; MUID:94083525; PMID:8260599  
A:Accession: I46046  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-204 <CL2>  
A:Cross-references: UNIPROT:Q06600; EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797  
C:Genetics:  
A:Introns: 32/3; 68/1  
C:Superfamily: tumor necrosis factor

Query Match 9.9%; Score 127.5; DB 1; Length 204;  
Best Local Similarity 24.9%; Pred. No. 0.0015;  
Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 61 TISTVQEQNISPLVRGQPVAAHITG-----TRGRSNTLSSPNSKNEKALGRKI 113  
Db 40 TPSAAQPAHQQL-PTPTFTRGTLPAAHLVGDPTQDSLWRANT-----DRAFLR-- 88

QY 114 NSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRFOEIKENTKDKQMVOYIY 173  
Db 89 -----HGF-----SLSNLSLVTSGLYFYISQVFSGRGCPFRATPTPLYLAHEVQ 135

QY 174 KYT-SYDPDPIILLMKARNSCWSKDAEYGLYSIYQGGIFELKENDRIFSVSTN-EHLIDMD 231  
Db 136 LFSPQVFFHPLLSAQKSCVCPGQGPW-VRSVYQGAFFLLTRGDQLSTHTDGSILL-LS 193

QY 232 HEASFFGAF 240  
Db 194 PSSVFFGAF 202

RESULT 12  
JQ1344  
tumor necrosis factor alpha precursor - horse  
N:Alternate names: cachectin; TNF alpha  
C:Species: Equus caballus (domestic horse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: JQ1344  
R:Su, X.; Morris, D.D.; McGraw, R.A.  
Gene 107, 319-321, 1991  
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f  
A:Reference number: JQ1344; MUID:92084125; PMID:1748301  
A:Accession: JQ1344  
A:Molecule type: DNA  
A:Residues: 1-234 <SUX>

A:Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245  
C:Comment: This protein is an important proximal mediator of endotoxemia.  
C:Genetics:  
A:Gene: TNF-alpha  
A:Introns: 62/3; 79/1; 95/1  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb  
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
F:19,20/Binding site: myristate (lys) (covalent) #status predicted  
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:146-178/Disulfide bonds: #status predicted

Query Match 9.8%; Score 126; DB 1; Length 234;  
Best Local Similarity 22.5%; Pred. No. 0.0025;  
Matches 45; Conservative 35; Mismatches 72; Indels 48; Gaps 9;

QY 62 ISTVQEQKQ-----QNISPLVR-----ERGP-QRVAAHITGRGRSNTLSSPNSKNEKALG 110  
Db 56 IGPQREEQLPNAPFOSINPLAQTLRSSSRTPSDKPAHVVA-----NQPAEG 101

QY 111 RKINSWESSRSGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRFOEIKENTKDKQMVO 170  
Db 102 QL--QWLSGRANALLANGVKLTQNLVPLDGLYISQVLFKQ-----GCPSTH 150

QY 171 YIYKYT-----SYDPDPIILLMKARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIF 219  
Db 151 VLLTHTISRLVSYSPKSNLLSAIKSPCHTESPEQAEAKPWPYPIYLGGVFQLEKGDLS 210

QY 220 VSVTNEHLIDMDHEAS-FFG 238  
Db 211 ASINQPNYLDPAESGQVYFG 230

RESULT 13  
QWUHN  
tumor necrosis factor alpha precursor [validated] - human  
N:Alternate names: cachectin; TNFA  
C:Species: Homo sapiens (man)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 09-Jul-2004  
C:Accession: A93585; S36153; A9351; A44189; B61478; I53311; S62610; I54522; A01646; B23:  
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.  
Nucleic Acids Res. 13, 6361-6373, 1985  
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro  
A:Reference number: A93585; MUID:86016093; PMID:2995927  
A:Accession: A93585  
A:Molecule type: DNA  
A:Residues: 1-233 <NED>  
A:Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PJ  
R:Iris, F.J.W.; Bougueret, L.; Frieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka,  
Nature Genet. 3, 137-145, 1993  
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a  
A:Reference number: S36152; MUID:93272029; PMID:8499947  
A:Accession: S36153  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-233 <NED>  
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992  
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.,  
Nature 312, 724-729, 1984  
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to l  
A:Reference number: A93351; MUID:85086244; PMID:6392892  
A:Accession: A93351  
A:Molecule type: mRNA  
A:Residues: 1-233 <PEN>  
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;  
Science 228, 149-154, 1985  
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
A:Reference number: A44189; MUID:85142190; PMID:3856324  
A:Accession: A44189  
A:Molecule type: mRNA



A;Accession: S03791  
A;Molecule type: DNA  
A;Residues: 1-235 <SHA>  
A;Cross-references: GB:M38296; NID:G202086; PIDN:AAA40459.1; PID:G202087  
A;Note: article in Russian with English abstract  
R;Samon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.  
Nucleic Acids Res. 15, 9083-9084, 1987  
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necrosis factor) gene  
A;Reference number: A93679; MUID:88067722; PMID:3684584  
A;Accession: A27303  
A;Molecule type: DNA  
A;Residues: 1-235 <SEN>  
A;Cross-references: GB:Y00467; NID:G54830; PIDN:CAA69530.1; PID:G54832  
R;Pennica, D.; Hayflick, J.S.; Brimman, T.S.; Palladino, M.A.; Goeddel, D.V.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985  
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor  
A;Reference number: A25164; MUID:85298296; PMID:3898078  
A;Accession: A25164  
A;Molecule type: mRNA  
A;Residues: 1-235 <PEN>  
A;Cross-references: GB:ML1731; NID:G202084; PIDN:AAA40458.1; PID:G202085  
R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, E.  
Nucleic Acids Res. 13, 4417-4429, 1985  
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression  
A;Reference number: A23127; MUID:85242112; PMID:2989794  
A;Accession: A23127  
A;Molecule type: mRNA  
A;Residues: 1-235 <FRA>  
A;Cross-references: GB:X02611; NID:G54844; PIDN:CAA26457.1; PID:G54845  
R;Caesh, K.; Beutler, B.  
J. Biol. Chem. 264, 16256-16260, 1989  
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in two different mature proteins  
A;Reference number: A34251; MUID:89380231; PMID:2777790  
A;Accession: A34251  
A;Molecule type: protein  
A;Residues: 70-87 <CSE>  
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region of the mouse cachectin and human tumor necrosis factor genes  
A;Reference number: I59058; MUID:86149365; PMID:2419912  
A;Accession: I59058  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-230,'R',232-235 <RES>  
A;Cross-references: GB:ML1049; NID:G202082; PIDN:AAA40457.1; PID:G202083  
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor  
A;Reference number: A36696; MUID:91097531; PMID:2268312  
A;Accession: A36696  
A;Molecule type: protein  
A;Residues: 80-85,'X',87-99 <SHE>  
C;Genetics:  
A;Introns: 62/3; 81/1; 97/1  
A;Note: the first intron occurs in the 5'-untranslated region  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein  
F;80-235/Product: tumor necrosis factor #status experimental <NAT>  
F;20/Binding site: myristate (lys) (covalent) #status predicted  
F;84/Binding site: carboxylate (Ser) (covalent) #status predicted  
F;86/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;148-179/Disulfide bonds: #status predicted

Query Match	9.4%	Score 121;	DB 1;	Length 235;
Best Local Similarity	23.1%;	Pred. No. 0.0066;		
Matches	43;	Conservative 34;	Mismatches 79;	Indels 30; Gaps 8;
Qy	67	EKQNIPLVREGRQPVAAHITGTRGSNTLSSP-----NSKNEKALGRKINSVSSR	120	
Db	62	EKFPNGIPLI-----SSMAQTILTRSSQNSDKPVAAHVAAHQVEEQI-----EMLSQR	111	
Qy	121	SGHSFLNLHLRNLGELVTHEKGFYYIYSQTYFRQFEIKENTKDKQMVOYIYKYT-SYP	179	

Db 112 ANALLANGMDLKNQJVPADGLYLVSQVLFKGQ-----GCPDYVLLTHTVSRFAISYQ 166  
Qy 180 DPILLMKSARNSCWSKDAEYG-----LYSIYGGIFELKENDRIFVSVTNEHLIDMDHE 233  
Db 167 EKVNLLSAVKSPC-PKOTPEGAELKPWYEFYILGGVFQLEKGDQLSAEVLNPKYLDPAES 225  
Qy 234 AS-FFG 238  
Db 226 GQVYFG 231

Search completed: June 22, 2005, 06:03:13  
Job time : 24.187 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 100.168 Seconds  
(without alignments)  
1242.266 Million cell updates/sec

Title: US-10-662-429-2\_COPY\_39\_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSKSGTACFL.....NEHLIDMDHEASFGAPLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1287	100.0	281	1	TN10_HUMAN	P50591 homo sapien
2	879	68.3	287	2	Q8K3G0	Q8K390 rattus norv
3	863	67.1	291	1	TN10_MOUSE	P50592 mus.musculu
4	703.5	54.7	304	2	Q7T1F2	Q7T1F2 gallus gall
5	515.5	40.1	299	2	Q6DHG9	Q6dhg9 brachydanio
6	307.5	23.9	317	2	Q7ZVX9	Q7zv99 brachydanio
7	305.5	23.7	214	2	Q9DDZ5	Q9ddz5 brachydanio
8	305	23.7	287	2	Q90WT9	Q90wt9 gallus gall
9	291	22.6	63	2	Q6JSD9	Q6jds9 homo sapien
10	250.5	19.5	318	1	TN11_RAT	Q9e8e2 r tumor nec
11	238.5	18.5	316	1	TN11_MOUSE	O14788 h tumor nec
12	235.5	18.3	317	1	TN11_HUMAN	P41047 mus musculu
13	189.5	14.7	279	1	TN10_MOUSE	Q9bnd1 cercocebus
14	185.5	14.4	280	1	TN10_MOUSE	Q7tmv9 mus musculu
15	184.5	14.3	279	2	Q7TMV9	P63308 macaca fasc
16	183.5	14.3	280	1	TN10_MOUSE	P63307 macaca mela
17	183.5	14.3	280	1	TN10_MOUSE	P63306 macaca mela
18	183.5	14.3	280	1	TN10_MOUSE	P48023 homo sapien
19	182.5	14.2	281	1	TN10_MOUSE	Q9bea8 sus scrofa
20	182	14.1	282	1	TN10_MOUSE	Q8K3Y8 mus musculu
21	180	14.0	252	2	Q8K3Y8	P36940 rattus norv
22	177.5	13.8	278	1	TN10_MOUSE	Q861w5 felis silve
23	176.5	13.7	280	2	Q861W5	Q9wv90 marmota mon
24	175.5	13.6	169	2	Q9WV90	Q80yz0 mus musculu
25	175	13.6	252	2	Q80VZ0	Q8K3Y7 rattus norv
26	173	13.4	252	2	Q8K3Y7	Q918d8 gallus gall
27	171	13.3	272	1	TN10_MOUSE	Q9nfe9 homo sapien
28	166	12.9	251	2	Q8NFE9	O613o6 canis famil
29	163.5	12.7	131	2	Q6J3O6	Q95130 homo sapien
30	160	12.4	174	1	TN15_HUMAN	O43557 homo sapien
31	159.5	12.4	240	1	TN15_HUMAN	

## RESULT 1

TN10_HUMAN	TN10_HUMAN	STANDARD;	PRT;	281 AA.
AC	P50591;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).			
DE	Name=TNFSF10; Synonyms=APO2L, TRAIL;			
GN	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OC	NCBI_TaxID=9606;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;			
RX	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,			
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,			
RA	Goodwin R.G.;			
RT	"Identification and characterization of a new member of the TNF family that induces apoptosis."			
RT	Immunology 3:673-682(1995).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Placenta;			
RC	MEDLINE=96278649; PubMed=8663110; DOI=10.1074/jbc.271.22.12687;			
RX	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,			
RA	Ashkenazi A.;			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."			
RT	J. Biol. Chem. 271:12687-12690(1996).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Lymph;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,			
RA	Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			

Q8mj19 macaca mula  
Q9qy99 mus musculu  
P51749 bos taurus  
Q7t2g3 cyprinus ca  
O70332 mesocricetu  
Q6u817 lateolabrax  
Q8aw02 cyprinus ca  
Q9bnd3 actus trivi  
Q9bnd3 callithrix  
Q80x84 peromyscus  
Q6t9c7 brachydanio  
P27548 mus musculu  
P63305 cercocebus  
P29965 homo sapien

## ALIGNMENTS



RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.  
RX MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;  
RA Hymowitz S.G., Christinger H.W., Fuh G., Uitsch M., O'Connell M.,  
RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
RL complex with death receptor 5.";  
RL Mol. Cell 4:563-571(1999).  
RN [5]  
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.  
RP PubMed=10542098; DOI=10.1038/14935;  
RX Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
RA Jones E.Y., Screaton G.R.;  
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
RL specificity in apoptotic initiation.";  
RL Nat. Struct. Biol. 6:1048-1053(1999).  
RN [6]  
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.  
RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;  
RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,  
RA Sung Y.C., Oh B.-H.;  
RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with  
RL selective antitumor activity.";  
RL Immunity 11:253-261(1999).  
CC -I- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,  
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and  
CC possibly also to TNFRSF1B/OPG. Induces apoptosis. Its activity  
CC may be modulated by binding to the decoy receptors  
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF1B/OPG that cannot  
CC induce apoptosis.  
CC -I- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per  
CC trimer.  
CC -I- SUBUNIT: Homotrimer.  
CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
CC -I- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung  
CC and prostate.  
CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.  
CC -----  
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CC -----  
DR EMBL; U37518; AAC50332.1; -;  
DR EMBL; U57059; AAB01233.1; -;  
DR EMBL; BC032722; AAH32722.1; -;  
DR PDB; 1D0G; X-ray; A/B/D=114-281.  
DR PDB; 1D2Q; X-ray; A=114-281.  
DR PDB; 1D4V; X-ray; B=119-281.  
DR PDB; 1D66; X-ray; A=91-281.  
DR PDB; 1DQ3; X-ray; D/E/F/G/K/L=114-281.  
DR Genew; HGNC:11925; TNFSF10.  
DR H-InvDB; HIX0003863; -;  
DR MIM; 603598; -;  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0005625; C:soluble fraction; TAS.  
DR GO; GO:0005102; F:receptor binding; TAS.  
DR GO; GO:0007267; P:cell-cell signaling; TAS.  
DR GO; GO:0006917; P:induction of apoptosis; TAS.  
DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IEP.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR008983; TNF-like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS0049; TNF 2; 1.  
KW 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;  
Transmembrane; Zinc.  
FT DOMAIN 1 17 Cytoplasmic (Potential).  
FT TRANSMEM 18 38 Signal-anchor for type II membrane  
protein (Potential).  
FT DOMAIN 39 281 Extracellular (Potential).  
FT METAL 230 230 Zinc.  
FT STRAND 123 127  
FT STRAND 149 150  
FT STRAND 163 165  
FT STRAND 167 170  
FT TURN 171 172  
FT STRAND 173 176  
FT STRAND 180 193  
FT TURN 198 199  
FT STRAND 205 213  
FT STRAND 220 228  
FT TURN 233 234  
FT STRAND 237 250  
FT TURN 252 253  
FT STRAND 255 260  
FT HELIX 263 265  
FT STRAND 266 267  
FT TURN 270 272  
FT STRAND 274 279  
SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;  
Query Match 100.0%; Score 1287; DB 1; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TNELQMODKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLTSEE 60  
DB 39 TNELQMODKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLTSEE 98  
QY 61 TISTVQEKQONISPLVRERGPOVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 120  
DB 99 TISTVQEKQONISPLVRERGPOVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 158  
QY 121 SGHSFLSNLHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQVYIKYTSYD 180  
DB 159 SGHSFLSNLHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQVYIKYTSYD 218  
QY 181 PILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAF 240  
DB 219 PILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAF 278  
QY 241 LVG 243  
DB 279 LVG 281  
RESULT 2  
Q8K3G0 PRELIMINARY; PRT; 287 AA.  
ID Q8K3G0  
AC Q8K3G0; DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE TNF-related apoptosis inducing ligand.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DA;  
RA Mueller A.M., Giegerich G.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY115578; AAM49797.1; -;  
DR HSSP; P50591; 1DQ.  
DR GO; GO:0016020; C:membrane; IEA.



DR GO: GO:0005164; P: tumor necrosis factor receptor binding; IEA.  
 DR GO: GO:0006955; P: immune response; IEA.  
 DR InterPro: IPR006032; TNF family.  
 DR InterPro: IPR008983; TNF like.  
 DR InterPro: IPR003636; TNF\_subf.  
 DR Pfam: PF00229; TNF; 1.  
 DR ProDom: PD002012; TNF\_subf; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF; 1; UNKNOWN\_1.  
 DR PROSITE: PS0049; TNF; 2; 1.  
 DR SEQUENCE 287 AA; 33979 MW; CA4F5B5D7C933PEC CRC64;  
 Query Match 68.3%; Score 879; DB 2; Length 287;  
 Best Local Similarity 69.7%; Pred. No. 5.2e-64;  
 Matches 170; Conservative 25; Mismatches 43; Indels 6; Gaps 2;  
 QY 2 NELKQMDKYSGKGIACFLKEDDSYDPNDDESMNSPCWQVQWQLRQLVRKMLRTSEET 61  
 Db 44 NEVKQLQDNYSKIGLACFSKDEGDFWSDTDEGLNRPCLQVQRQLYLTIEVLTFTFEK 103  
 QY 62 ISTVQEKQONISPLVREGRQPVAAHITGTRGRSNTLSSPNKVEKALGRKINSWESSR 121  
 Db 104 ISTVPEKQLSTPPLPRGRRPQVAAHITGTRSNLALIPISKDGLTQGIETWESSR 163  
 QY 122 GHSFLNLHLNGLVHEKGYIYSQTYFRQES--EIKENTKND-----KQWVQYIYKY 175  
 Db 164 GHSFLNLHLNGLVHEKGYIYSQTYFRQES--EIKENTKND-----KQWVQYIYKY 223  
 QY 176 TSYPDPIILLKMSARNCSWDAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEAS 235  
 Db 224 TSYPDPIILLKMSARNCSWDAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEAS 283  
 QY 236 FFGA 239  
 Db 284 FFGA 287  
 RESULT 3  
 TN10\_MOUSE STANDARD; PRT; 291 AA.  
 AC P50592;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related  
 apoptosis inducing ligand) (TRAIL protein).  
 GN Name=TNFsf10; Synonyms=Trail;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;  
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,  
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C.A.,  
 RA Goodwin R.G.;  
 RT Identification and characterization of a new member of the TNF family  
 that induces apoptosis.  
 RL Immunity 3:673-682(1995).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1.  
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and  
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity  
 CC may be modulated by binding to the decoy receptors  
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot  
 CC induce apoptosis.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Widespread.  
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: U37522; AAC52345.1; --  
 DR HSSP: P50591; 1D2Q.  
 DR MG: MG1:107414; Tnf9f10.  
 DR InterPro: IPR006032; TNF family.  
 DR InterPro: IPR008983; TNF like.  
 DR InterPro: IPR003636; TNF\_subf.  
 DR Pfam: PF00229; TNF; 1.  
 DR ProDom: PD002012; TNF\_subf; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF; 1; 1.  
 DR PROSITE: PS0049; TNF; 2; 1.  
 KW Apoptosis; Cytokine; Signal-anchor; Cytoplasmic (Potential).  
 FT DOMAIN 1 17 Cytoplasmic (Potential).  
 FT TRANSMEM 18 38 Signal-anchor for type II membrane  
 FT DOMAIN 39 291 Extracellular (Potential).  
 FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;  
 Query Match 67.1%; Score 863; DB 1; Length 291;  
 Best Local Similarity 66.1%; Pred. No. 1.1e-62;  
 Matches 164; Conservative 32; Mismatches 46; Indels 6; Gaps 1;  
 QY 1 TNELKQMDKYSGKGIACFLKEDDSYDPNDDESMNSPCWQVQWQLRQLVRKMLRTSE 60  
 Db 43 TNELKQMDKYSGKGIACFLKEDDSYDPNDDESMNSPCWQVQWQLRQLVRKMLRTSE 102  
 QY 61 TISTVQEKQONISPLVREGRQPVAAHITGTRGRSNTLSSPNKVEKALGRKINSWESSR 120  
 Db 103 TISTVPEKQLSTPPLPRGRRPQVAAHITGTRSNLALIPISKDGLTQGIETWESSR 162  
 QY 121 GHSFLNLHLNGLVHEKGYIYSQTYFRQES--EIKENTKNDKQWVQYIYKY 174  
 Db 163 GHSFLNLHLNGLVHEKGYIYSQTYFRQES--EIKENTKNDKQWVQYIYKY 222  
 QY 175 YTSYDPPIILLKMSARNCSWDAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEA 234  
 Db 223 YTSYDPPIILLKMSARNCSWDAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEA 282  
 QY 235 SFFGAFLV 242  
 Db 283 SFFGAFLI 290  
 RESULT 4  
 Q7TIF2 PRELIMINARY; PRT; 304 AA.  
 ID Q7TIF2;  
 AC Q7TIF2;  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Tumor necrosis factor related apoptosis inducing ligand.  
 GN Name=TRAIL;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Splice;  
 RA Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;  
 RT "Molecular Cloning and Characterization of Chicken Tumor Necrosis  
 RT Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis  
 RT Inducing Ligand (TRAIL).";  
 RL J. Vet. Med. Sci. 66:643-650(2004).  
 DR EMBL: AB114678; BAC79267.1; --

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DR HSP; P50591; 1D2Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.7%; Score 703.5; DB 2; Length 304;
Best Local Similarity 54.7%; Pred. No. 1.4e-49;
Matches 141; Conservative 40; Mismatches 58; Indels 19; Gaps 6;

QY 1 TNELKQMDKYKSGIACFLKEDSDSYWDPN-----DESMNSPCWQVQWQLRQLVRKML 55
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
36 TNELKQLWDYTSRSGTACLTGELGLDQLNLDVVEKDRVADPCWQVQWHLGKLKQWMS 95
QY 56 RISEETISTVQ-EKQNIQPLVRGPQ-----RVAHIITGTRGRSNTLSSPNSKNEKALG 110
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 RILQENMSAINGDRTQALSR--RDEPPQGTLLRIAAHLTGSSKRSSA-SPHNYLSYRGIG 152
QY 111 RKNWESSRSGHSFLSNLHRLNGELVHIEKGFYIYSQTYFRFOE-----IKENTKN 164
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
153 HKIHWESSRRGHSFLYNVELNGELVLPQTGFYIYSQTYFRFNEDEDSGLLERIKN 212
QY 165 DKQWQYIYKYTSYPPDILLMKSAKNSCWDAEYGLYSYQGGIFELKENDRIFVSVTN 224
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
213 PRQLVQYIKLTNPDPILLMKSAKNSCWDAEYGLYSYQGGIFELKENDRIFVSVN 272
QY 225 EHLIDMDHEASFFGAPLV 242
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
273 SDIVDMDKESFFGAPFI 290

RESULT 5
Q6DHG9 PRELIMINARY; PRT; 299 AA.
AC Q6DHG9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:92320.
GN Name=zgc:92320;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinska M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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QY 65 VQKQ---NISP-LVRGPQVAAH-----TGTGRSNTLSPNSKNEKALGR 111
DB 103 VNEAQKSYENISGGVATKTLGKPSAHLIFRPNQPAQDSSRRFGNLS-----QSCRH 155
QY 112 KINSWSSRGHSFLNLHLRNGELVIHEKGFYIYSQYFRQBEIKENTKNDKQVQY 171
DB 156 AITRWEDS-TIHLQNTITRDGLRVNQAGKYVYSQIYFRYSRDGAGARVSPQLVQC 214
QY 172 IYKTSYPPDILLMKSNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMD 231
DB 215 INWKTSYDIPILLKGVGKYCAPEAYEYGLHLYQGLFELKAGDELFSVSSLAIDYSD 274
QY 232 HEASFFGAF 240
DB 275 AASYFGAF 283

RESULT 9
Q6JSD9 PRELIMINARY; PRT; 63 AA.
AC O6JSD9
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Chemokine tumor necrosis factor ligand superfamily member 10
DE (Fragment)
GN Name=TNFSF10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
RA Reinikainen A., Hollmen J., Laitinen T., Mannila H., Laheesmaa R.,
RA Kere J.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AV312579; AAR16184.1; -.
FT NON_TER 1 1
SQ SEQUENCE 63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;

Query Match 22.6%; Score 291; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYNDPNDESMNSPCWQVKWQLRQLVRK 52
DB 1 TNELKQMDKYKSGIACFLKEDDSYNDPNDESMNSPCWQVKWQLRQLVRK 52

RESULT 10
TN11 RAT STANDARD; PRT; 318 AA.
AC Q9SE2; Q91219;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE differentiation factor) (ODF).
GN Name=TNfrsf11; Synonyms=Oppl, Rankl, Trance;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tibial bone;
RX MEDLINE=20540945; PubMed=11092398;
RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,

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RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RT homologue of receptor activator of NF-kB ligand.";
RL J. Bone Miner. Res. 15:2178-2186(2000).
RN [2]
RP SEQUENCE OF 266-318 FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=21662371; PubMed=11804028;
RA Odgren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savas A.,
RA Safadi P.P., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
RA Marks S.C. Jr.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
RL Int. J. Dev. Biol. 45:853-859(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
DR EMBL: AF187319; AAG17031.1; -.
DR EMBL: AF425669; AAL23963.1; -.
DR KSSP: OJ5235; 1JTZ.
DR GSD; 620784; tnfsf11.
DR InterPro: IPR006052; TNF family.
DR InterPro: IPR008983; TNF_like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF_subf; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; FALSE_NEG.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;
KW Transmembrane.
FT CHAIN 1 318 Tumor necrosis factor ligand superfamily
FT member 11, membrane form.
FT CHAIN 141 318 Tumor necrosis factor ligand superfamily
FT member 11, soluble form.
FT DOMAIN 1 47 Cytoplasmic (Potential).
FT TRANSMEM 48 68 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 69 318 Extracellular (Potential).
FT SITE 140 141 Cleavage (By similarity).
FT CARBOHYD 199 199 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 264 264 N-linked (GlcNAc...) (Potential).
FT CONFLICT 317 317 I -> M (in Ref. 2).
SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

Query Match 19.5%; Score 250.5; DB 1; Length 318;
Best Local Similarity 28.5%; Pred. No. 2.4e-12;
Matches 75; Conservative 46; Mismatches 87; Indels 55; Gaps 10;

QY 9 DKYSKGIACF-----LKED----DSYNDPNDESMNSPCWQVKWQLRQLVRKLTSE 59
DB 78 NRISDSTCFYRLRLRENTGLQDSTLESEDEALPDSCRWKQAFQ----- 125

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QY 60 ETISTVQKQNTSPLVRGPOR---VAAHITGT-----RGRS-----NTLSS 100  
 DB 126 ---GAVQRELQHV-----GPRFSGVPANMEGSLDVARKGPEAQPPFAHLTINADI 176  
 QY 101 PNSNKALGRKINSMESSRSHGSHFSLNHLRNGELVIHKGFGYIYISQTYFRFQEBIKE 160  
 DB 177 PSQSHKVSU-----SSWYHDR-GWAKISNMTLSNKLKRVNQDGFYLYANICFRHETSQS 231  
 QY 161 NTQNDQKQWQYIYKT-SYDDPILLMKSAKNSCWDAEGLVSIYGGIFELKENDRIF 219  
 DB 232 VPADYLQLMVYVVKTSIKPSSHNLMKGGSTKQNSGSEFHFYSINVGGFFKLKRGEBIS 291  
 QY 220 VSVTNEHLIDMDHEASFFGAFLV 242  
 DB 292 VQVSNFSLDPDQDQATYFGAKV 314

RESULT 11

TN11\_MOUSE STANDARD; PRT; 316 AA.  
 AC Q35235; Q35306; Q9JUK8; Q9JUK9; Q9RIY0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)  
 DE (OCIF).  
 GN Names=Tnfsl1; Synonyms=OPGL, RANKL, Trance;  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Hybridoma;  
 RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;  
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,  
 RA Kalachikov S., Cayani E., Bartlett P.S. III, Frankel W.N., Lee S.Y.,  
 RA Choi Y.;  
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells.";  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Thymic lymphoma;  
 RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;  
 RA Anderson D.W., Maraskovsky E., Billingsley W.B., Dougall W.C.,  
 RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
 RA Galibert L.;  
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;  
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
 RA Boyle W.J.;  
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
 RT differentiation and activation.";  
 RL Cell 93:165-176(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow stroma;  
 RX MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;  
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,  
 RA Mochizuki S.-I., Tomoyasu A., Iano K., Goto K., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
 RT "Osteoclast differentiation factor is a ligand for  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical  
 RT to TRANCE/RANKL.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=129;  
 RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;  
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,  
 RA Ueda M., Higashio K.;  
 RT "Cloning and characterization of the gene encoding mouse osteoclast  
 RT differentiation factor.";  
 RL Gene 230:121-127(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;  
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;  
 RT "Determination of three isoforms of the receptor activator of nuclear  
 RT factor-kappaB ligand and their differential expression in bone and  
 RT thymus.";  
 RL Endocrinology 142:1419-1426(2001).  
 RN [7]  
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.  
 RX MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;  
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,  
 RA Schluender P., Tempst P., Choi Y., Blobel C.P.;  
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-  
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family  
 RT member involved in osteoclastogenesis and dendritic cell survival.";  
 RL J. Biol. Chem. 274:13613-13618(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.  
 RX MEDLINE=21464816; PubMed=11581298;  
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;  
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants  
 RT of receptor-ligand specificity.";  
 RL J. Clin. Invest. 108:971-979(2001).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.  
 RX MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;  
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;  
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at  
 RT 2.2-A resolution.";  
 RL J. Biol. Chem. 277:6631-6636(2002).  
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcaemia of malignancy.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted  
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O35235-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O35235-2; Sequence=VSP\_006449;  
 CC Name=3;  
 CC IsoId=O35235-3; Sequence=VSP\_006448;  
 CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,  
 CC but not in nonlymphoid tissues and is abundantly expressed in T  
 CC cells but not in B cells. A high level expression is also seen in  
 CC the trabecular bone and lung.  
 CC -1- PTM: N-glycosylated.  
 CC -1- PTM: The soluble form of isoform 1 derives from the membrane form  
 CC by proteolytic processing. The cleavage may be catalyzed by  
 CC ADAM17. A further shorter soluble form was observed.  
 CC -1- DISEASE: Deficiency in tnfrsf11 results in failure to form lobulo-





RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;  
 RA Wong B R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., S.Y.,  
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
 RA Choi Y.;  
 RT "TRANSC is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells.";  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [5];  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=tongue;  
 RA MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;  
 RA Nagai M., Kyakumoto S., Sato N.;  
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA  
 RT encoding a secreted form of ODF/TRANSC that induces osteoclast  
 RT formation.";  
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).  
 CC -I- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -I- SUBUNIT: Homotrimer (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);  
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by  
 CC proteolytic processing (By similarity).  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O14788-1; Sequence=Displayed;  
 CC Name=2; Synonyms=SODF;  
 CC IsoId=O14788-2; Sequence=VSP\_006447;  
 CC Name=3;  
 CC IsoId=O14788-3; Sequence=VSP\_006446;  
 CC -I- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in  
 CC spleen, peripheral blood leukocytes, bone marrow, heart, placenta,  
 CC skeletal muscle, stomach and thyroid.  
 CC -I- INDUCTION: Up-regulated by T cell receptor stimulation.  
 CC -I- PTM: The soluble form of isoform 1 derives from the membrane form  
 CC by proteolytic processing (By similarity). The cleavage may be  
 CC catalyzed by ADAM17.  
 CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 CC EMBL; AF019047; AB86811.1; -;  
 CC EMBL; AF053712; AAC39731.1; -;  
 CC EMBL; AB064269; BAB79694.1; -;  
 CC EMBL; AB061227; BAB71768.1; -;  
 CC EMBL; AB064270; BAB79695.1; -;  
 CC EMBL; AF013171; AAC51762.1; -;  
 CC EMBL; AB037599; BAA90488.1; -;  
 CC HSSP; O35235; IJTZ.  
 CC Genew; HGNC:11926; TNFSF11.  
 CC MIM; 602642; -;  
 CC GO; GO:0005576; C:extracellular; NAS.  
 CC GO; GO:0005887; C:integral to plasma membrane; NAS.  
 CC GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.  
 CC GO; GO:0006955; P:immune response; NAS.  
 CC GO; GO:0030316; P:osteoclast differentiation; NAS.  
 CC InterPro; IPR006052; TNF family.  
 CC InterPro; IPR008983; TNF-like.  
 CC InterPro; IPR003636; TNF\_subf.  
 CC Pfam; PF00229; TNF; 1.  
 CC ProDom; PD002012; TNF\_subf; 1.

DR SMART: SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 DR PROSITE; PS00049; TNF\_2; 1.  
 KW Alternative splicing; Cytokine; Differentiation; Glycoprotein;  
 KW Receptor; Signal-anchor; Transmembrane.  
 FT CHAIN 1 317  
 FT member 11, membrane form.  
 FT CHAIN 140 317  
 FT member 11, membrane form.  
 FT Tumor necrosis factor ligand superfamily  
 FT member 11, soluble form (By similarity).  
 FT CYTOPLASMIC (Potential).  
 FT Signal-anchor for type II membrane  
 FT protein (Potential).  
 FT Extracellular (Potential).  
 FT Cleavage (By similarity).  
 FT SITE 139 140  
 FT CARBOHYD 171  
 FT CARBOHYD 198 198  
 FT N-linked (GlcNAc...) (Potential).  
 FT VARSPLIC 1 47  
 FT Missing (in isoform 3).  
 FT FTId=VSP\_006446.  
 FT VARSPLIC 1 73  
 FT Missing (in isoform 2).  
 FT FTId=VSP\_006447.  
 FT CONFLICT 194 194  
 FT A -> G (in Ref. 4).  
 SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;  
 Query Match 18.3%; Score 235.5; DB 1; Length 317;  
 Best Local Similarity 25.3%; Pred. No. 4.1e-11;  
 Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;  
 QY 9 DKYSGGIACF-----LKED----DSYMDPNDSESMNSPCWQVKW-----QLRQLVR 51  
 DB 77 NRISDGTCHIVRLLEHENADPDYTLSDTKLPDSCRRKIQAFQGVQKELHIVG 136  
 QY 52 KMLRTSEETI-----STVOEKQONISPLVRGPGORVAHITGTRGNTLSPNSKNE 106  
 DB 137 SQHRAEKAMVDGSLDLAKRSKLEAQP-----AHLT-----INATDIPSGSHK 181  
 QY 107 KALGRKINSESRSHSPLNLHLNGLVTHEKGFYIYSQTYFRFOEIEIKENTKNDK 166  
 DB 182 VSL-----SSWYHNR-GWAKISNNTSGNKLIVNQDGFYLYANICFRHHTSGDLATEYL 236  
 QY 167 QMVOYIKYT-SYDPDPIILMKARNCSWKSADAEGLYSIVQGGIFELKENDRIFVSVTNE 225  
 DB 237 QLMVYVTKTSIKIPSSHTLMKGGSTKYNSGNSEFPFYSINVGFFKLRSGEISIEVSNP 296  
 QY 226 HLIDMDHEASFFGAFLV 242  
 DB 297 SLLDPDQDATYFGAFKV 313  
 RESULT 13  
 TNF6\_MOUSE  
 ID TNF6\_MOUSE STANDARD; PRT; 279 AA.  
 AC P41047; O61217; Q9R1F2;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen  
 DE ligand).  
 GN Names=Tnf6; Synonyms=APRILG1, FasL, gld;  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL).  
 RX MEDLINE=94185175; PubMed=7511063; DOI=10.1016/0092-8674(94)90375-1;  
 RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,  
 RA Suda T., Nagata S.;  
 RT "Generalized lymphoproliferative disease in mice, caused by a point  
 RT mutation in the Fas ligand";  
 RL Cell 76:969-976(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.  
 RC STRAIN=C57BL/6;

RX MEDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;  
RA Peitech M.J., Tschopp J.J.;  
RT "Comparative molecular modelling of the Fas-ligand and other members  
RL of the TNF family."; Mol. Immunol. 32:761-772(1995).  
RN [3]  
RN SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106-6;  
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
RN Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF  
RL family gene cluster."; Immunol. 113:131-136(1994).  
RN [4]  
RN SEQUENCE FROM N.A. (ISOFORM FASL).  
RX STRAIN=BALB/c;  
RA Penner M.H., Shioda T., Isselbacher K.J.;  
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two  
RL amino acids."; Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RN SEQUENCE FROM N.A. (ISOFORM FASL).  
RX STRAIN=C3H; TISSUE=Spleen;  
RA MEDLINE=20021694; PubMed=10552956;  
RA Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,  
RN Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;  
RT "Cloning and expression of a short Fas ligand: a new alternatively  
RL spliced product of the mouse Fas ligand gene."; Blood 94:3456-3467(1999).  
RN [6]  
RN CHARACTERIZATION OF VARIANT GLD.  
RX MEDLINE=96091792; PubMed=7495745;  
RA Habne M., Peitech M.C., Irmiler M., Schroeter M., Lowin B.,  
RN Rousseau M., Bron C., Renno T., Frensch L., Tschopp J.;  
RT "Characterization of the non-functional Fas ligand of gld mice."; Int. Immunol. 7:1381-1386(1995).  
RN [7]  
RN VARIANTS ALA-184 AND GLY-218.  
RX STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and  
RN SUL;  
RX MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;  
RA Kayaagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,  
RN Yagita H.;  
RT "Polymorphism of murine Fas ligand that affects the biological  
RL activity."; Acad. Sci. U.S.A. 94:3914-3919(1997).  
RN Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).  
CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
CC transduces the apoptotic signal into cells. May be involved in  
CC cytotoxic T cell mediated apoptosis and in T cell development.  
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
CC peripheral tolerance, in the antigen-stimulated suicide of mature  
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3  
CC modulates its effects (By similarity).  
CC -1- SUBUNIT: Homotrimer (Probable).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);  
CC Secreted (isoforms FASL and FASLS).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=FasL;  
CC IsoId=P41047-1; Sequence=Displayed;  
CC Name=FasLS;  
CC IsoId=P41047-2; Sequence=VSP\_006445;  
CC -1- PTM: The soluble form derives from the membrane form by  
CC proteolytic processing (By similarity).  
CC -1- DISEASE: A deficiency in this protein is the cause of generalized  
CC lymphoproliferation disease phenotype (gld). Gld mice present  
CC lymphadenopathy and autoantibody production. The phenotype is  
CC recessively inherited.  
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; U06948; AAA17800.1; -  
DR EMBL; U10984; AAA19778.1; -  
DR EMBL; S76752; AAB33780.1; -  
DR EMBL; U58995; AAB02915.1; -  
DR EMBL; AF119335; AAD52106.1; -  
DR PIR; A53062; A53062.  
DR HSP; P50591; I066.  
DR MGD; MGI:99255; tnfsf6.  
DR InterPro; IPR008064; Fas ligand.  
DR InterPro; IPR006053; TNF abc.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR008983; TNF like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01681; FASLIGAND.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS00449; TNF\_2; 1.  
KW Alternative splicing; Apoptosis; Cytokine; Disease mutation;  
KW Glycoprotein; Polymorphism; Signal-anchor; Transmembrane.  
FT CHAIN 1 279  
FT CHAIN 128 279  
FT DOMAIN 1 78  
FT TRANSMEM 79 100  
FT DOMAIN 101 279  
FT DOMAIN 4 59  
FT DOMAIN 45 51  
FT SITE 127 128  
FT SITE 127 128  
FT DISULFID 200 231  
FT CARBOHYD 117 117  
FT CARBOHYD 182 182  
FT CARBOHYD 248 248  
FT CARBOHYD 258 258  
FT VARSPLIC 1 210  
FT VARIANT 184 184  
FT FTID=VSP\_006445.  
FT T -> A (in strain BALB/c, strain DBA/1  
FT and strain DBA/2; enhances cytotoxicity).  
FT E -> G (in strain BALB/c, strain DBA/1  
FT and strain DBA/2; enhances cytotoxicity).  
FT F -> L (in gld; abolishes binding of FASL  
FT to its receptor).  
SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;  
Query Match 14.7%; Score 189.5; DB 1; Length 279;  
Best Local Similarity 25.8%; Pred. No. 2.1e-07;  
Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;  
QY 45 QLRLVRKMLRTSETISTVQEKQONISPLVRERQPVAAHITGRGNTLSSPNSK 104  
Db 111 ELREFTNQSL-----KVSSPEKQIANPTPEKPRSV-AHLTG-----NPHSR 154  
QY 105 NEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKGYFYIYSQYFRFQEEIKENTKN 164  
Db 155 SIPL-----EWEDT-VGTALISGVKYGKGLVINETGLYFVYSKVYFRGQ-----SCN 201  
QY 165 DKQMVOYIY-KYTSYDPDILLMKSR-NSCWKSQDAEGLYSYQGGIFELKENDRIFVSV 222  
Db 202 NQPLNKHVYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSDHLYVNI 259  
QY 223 TNEHLIDMDHEASFFGCA 240  
Db 260 SLSLINFESKTFGLY 277

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-----



[illegible]



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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 108.052 Seconds  
(without alignments)  
869.796 Million cell updates/sec

Title: US-10-662-429-2\_COPY\_39\_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYKSGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	279	2	AAW76332 Human TL2
2	1287	100.0	279	2	AAW95032 Tumour ne
3	1287	100.0	281	2	AAW19777 Novel cyt
4	1287	100.0	281	2	AAW27134 Human Apo
5	1287	100.0	281	2	AAW19787 Human apo
6	1287	100.0	281	2	AAW76829 Human TL2
7	1287	100.0	281	2	AAW56760 Human TR4
8	1287	100.0	281	2	AAW44354 Human AGP
9	1287	100.0	281	2	AAW01517 Protein a
10	1287	100.0	281	2	AAW27012 Human Apo
11	1287	100.0	281	3	AAW81956 Human PRO
12	1287	100.0	281	3	AAW24038 Human PRO
13	1287	100.0	281	3	AAW08545 Amino aci
14	1287	100.0	281	3	AAW28691 Human AGP
15	1287	100.0	281	4	AAW50977 Human PRO
16	1287	100.0	281	4	AAW67243 Human Apo
17	1287	100.0	281	4	AAW11031 Human TNF
18	1287	100.0	281	4	AAW48350 Human TL2
19	1287	100.0	281	5	AAW08133 Human TRA
20	1287	100.0	281	5	AAW31630 Human TRA
21	1287	100.0	281	5	AAW75062 Human TNF
22	1287	100.0	281	5	AAW51077 Human Apo
23	1287	100.0	281	5	AAW51954 Human Apo
24	1287	100.0	281	5	AAW19095 C neoform
25	1287	100.0	281	5	AAW79593 Human TNF

26	1287	100.0	281	6	ABG73861	Abg73861 Human Apo
27	1287	100.0	281	6	ABU10205	Abu10205 Human Apo
28	1287	100.0	281	6	ABU71443	Abu71443 Human neo
29	1287	100.0	281	6	ABG72738	Abg72738 Human TNF
30	1287	100.0	281	6	AAO29543	Aao29543 Human TRA
31	1287	100.0	281	6	ABU08558	Abu08558 Human TNF
32	1287	100.0	281	6	ABR42313	AbR42313 Human TRA
33	1287	100.0	281	6	ABG71905	Abg71905 Human TRA
34	1287	100.0	281	6	ABP60546	Abp60546 Human tum
35	1287	100.0	281	6	AAE36258	Aae36258 Human TR4
36	1287	100.0	281	6	AAO31151	Aao31151 Human TNF
37	1287	100.0	281	6	ABO25125	AbO25125 Human TNF
38	1287	100.0	281	7	ADB61471	AdB61471 Native hu
39	1287	100.0	281	7	ADC35202	AdC35202 Human TNF
40	1287	100.0	281	7	ADD14080	Add14080 Human src
41	1287	100.0	281	7	ADD19010	Add19010 Human dis
42	1287	100.0	281	7	ABW02276	AbW02276 Human TRA
43	1287	100.0	281	8	ADE76953	AdE76953 Human pro
44	1287	100.0	281	8	ADK72311	AdK72311 Human Apo
45	1287	100.0	281	8	ADK72303	AdK72303 Human Apo

#### ALIGNMENTS

##### RESULT 1

AAW76332

ID AAW76332 standard; protein; 279 AA.

XX AC AAW76332;

XX XX 11-JAN-1999 (first entry)

XX DE Human TL2 (TRAIL), ligand for TR5.

XX KW TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation;

KW arthritis; septicemia; transplant rejection; autoimmune disease;

KW inflammatory bowel disease; graft versus host disease; infection; stroke;

KW ischaemia; acute respiratory disease syndrome; psoriasis; restenosis;

KW brain injury; AIDS; bone disease; cancer; atherosclerosis;

KW Alzheimer's disease; human; therapy; diagnosis; ligand.

XX OS Homo sapiens.

XX PN EP867509-A2.

XX PD 30-SRP-1998.

XX PF 04-FEB-1998; 98EP-00300827.

XX PR 05-FEB-1997; 97US-00795910.

XX PR 28-JUL-1997; 97US-00901469.

XX PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX PI Young PR, Tan KB, Truneh A, Lyn SDP;

XX DR WPI; 1998-497862/43.

XX PT New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent

PT and treat e.g. inflammation, arthritis, septicemia, autoimmune diseases,

PT infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,

XX AIDS and bone diseases.

XX PS Disclosure; Page 17-18; 22pp; English.

XX CC This is the amino acid sequence of human TL2 (also known as TRAIL), which

CC has newly been discovered to be a ligand of human tumour necrosis related

CC receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and

CC TL2 can be used in screening processes for compounds which bind the

CC receptor, or its ligand, and which activate (agonists) or inhibit

CC (antagonists) the receptor or TL2. Treatment of a subject with the need

CC to inhibit TR5 polypeptide activity comprises administering an antagonist

CC to the polypeptide, administering a nucleic acid that inhibits the  
CC expression of the nucleotide sequence encoding the polypeptide and/or  
CC administering a polypeptide that competes with the polypeptide for its  
CC ligand, substrate or receptor. The active agents can be used for the  
CC treatment of chronic and acute inflammation, arthritis, septicemia,  
CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),  
CC transplant rejection, graft vs host disease, infection, stroke,  
CC ischemia, acute respiratory disease syndrome, restenosis, brain injury,  
CC AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),  
CC atherosclerosis and Alzheimer's disease  
XX  
SQ Sequence 279 AA;

Query Match 100.0%; Score 1287; DB 2; Length 279;  
Best Local Similarity 100.0%; Pred. No. 3.4e-117;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQKQLRQVRKMLRTSEE 60  
DB 37 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQKQLRQVRKMLRTSEE 96  
QY 61 TISTVQEKQONISPLVRERGPORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
DB 97 TISTVQEKQONISPLVRERGPORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156  
QY 121 SGHSFLSNLHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 180  
DB 157 SGHSFLSNLHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 216  
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
DB 217 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276  
QY 241 LVG 243  
DB 277 LVG 279

RESULT 2  
AAW95032  
ID AAW95032 standard; protein; 279 AA.  
XX  
AC AAW95032;  
XX  
DT 13-MAY-1999 (first entry)  
XX  
DE Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.  
XX  
KW Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;  
KW inflammation; septicemia; autoimmune disease; transplant rejection;  
KW graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;  
KW acute respiratory disease syndrome; restenosis; bone disease; cancer;  
KW atherosclerosis; Alzheimer's disease.  
XX  
OS Unidentified.  
XX  
PN EP897114-A2.  
XX  
PD 17-FEB-1999.  
XX  
PF 04-JUN-1998; 98EP-00304424.  
XX  
PR 13-AUG-1997; 97US-0055513P.  
PR 26-AUG-1997; 97US-0056980P.  
PR 29-AUG-1997; 97US-0057550P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Brigham-Burke MR, Young PR;  
XX  
DR WPI; 1999-134308/12.  
XX  
PT Identifying agonists and antagonists to tumour necrosis factor receptor

PT (TNF-R) related polypeptides (LR1, LR2, LR2 and LT4) - useful for  
PT treating stroke, Alzheimer's disease and AIDS.  
XX  
PS Disclosure; Page 14-15; 18pp; English.  
XX  
CC The invention relates to identifying agonists or antagonists to tumour  
CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2  
CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a  
CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2  
CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)  
CC assessing the ability of the candidate compound to compete with TR1 or  
CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful  
CC for treating diseases caused by imbalance of TL or TR polypeptide levels,  
CC which cause: chronic and acute inflammation, arthritis, septicemia,  
CC autoimmune diseases, transplant rejection, graft vs. host disease,  
CC infection, stroke, ischemia, acute respiratory disease syndrome,  
CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and  
CC Alzheimer's disease. The present sequence represents a TNF-R related  
CC polypeptide TL2  
XX  
SQ Sequence 279 AA;

Query Match 100.0%; Score 1287; DB 2; Length 279;  
Best Local Similarity 100.0%; Pred. No. 3.4e-117;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQKQLRQVRKMLRTSEE 60  
DB 37 TNELKQMDKYKSGIACFLKEDDSYWDNDDESMNSPCWQKQLRQVRKMLRTSEE 96  
QY 61 TISTVQEKQONISPLVRERGPORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
DB 97 TISTVQEKQONISPLVRERGPORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156  
QY 121 SGHSFLSNLHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 180  
DB 157 SGHSFLSNLHLRNGELVTHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDP 216  
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
DB 217 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276  
QY 241 LVG 243  
DB 277 LVG 279

RESULT 3  
AAW19777  
ID AAW19777 standard; protein; 281 AA.  
XX  
AC AAW19777;  
XX  
DT 22-SEP-1997 (first entry)  
XX  
DE Novel cytokine Apo-2 ligand.  
XX  
KW Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Peptide 1..281  
FT Region 1..14  
FT Protein 15..281  
FT Region 15..40  
FT Protein 41..281  
FT Region 41..281  
Location/Qualifiers  
/note="Claim 4"  
/label="Cytoplasmic\_region"  
/note="Claim 3"  
/label="Transmembrane\_region"  
/note="Claim 2"

	/label= Extracellular_region
FT	Modified-site
XX	109
FT	/label= Glycosylation
FT	/note= "putative N-linked glycosylation site"
Protein	114.. .281
FT	/note= "Claim 1"
XX	
MW9725428-A1.	
PN	
17-JUL-1997.	
PP	
08-JAN-1997;	97WO-US000272.
XX	
PR	
09-JAN-1996;	96US-00584031.
XX	
(GETH ) GENENTECH INC.	
PA	
Ashkenazi AJ,	Chuntharapai A, Kim KJ;
Pt	
WIPI; 1997-372867/34.	
N-PSDB; AAAT72796.	
DR	
Noel cytokine, Apo-2 ligand and corresponding DNA - used to induce apoptosis for the treatment of breast and colon cancer.	
PT	
claim 4; Fig 1a; 72pp; English.	
PS	
A novel cytokine (AAW1977), designated Apo-2 ligand, induces mammalian cell apoptosis. It is believed to be a member of the tumour necrosis factor cytokine family. Its amino acid sequence was deduced from a cDNA clone (AAT72796) isolated from a human placental CDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic acid. They can be used to induce apoptosis in mammals and to treat pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays	
CC	
Sequence 281 AA;	
Query Match	100.0%; Score 1287; DB 2; Length 281;
Best Local Similarity	100.0%; Pred. No. 3.4e-117;
Matches 243; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TNELQMOMDKYSKSGIACFLKEDDSYWPNDDESMNSPCWKOLRLVRKMILRTSEE 60       39 TNELQMOMDKYSKSGIACFLKEDDSYWPNDDESMNSPCWKOLRLVRKMILRTSEE 98 
Dd	
QY	61 TISTVQEKOQNISPLVREGRGPORVAAHITGTRGNSTLSSPNSKNKEALGRKINSWEISSR 120       99 TISTVQEKOQNISPLVREGRGPORVAAHITGTRGNSTLSSPNSKNKEALGRKINSWEISSR 158 
Dd	
QY	121 SGHSFSLNHLNGELVLIVHEKGFFYYISQTYPFRFOEIKENTKDQKWVVIIKYTTSYPD 180       159 SGHSFSLNHLNGELVLIVHEKGFFYYISQTYPFRFOEIKENTKDQKWVVIIKYTTSYPD 218 
Dd	
QY	181 PILLMKASRNCSCKSDAEYGLYSIYGCGIFELKENDRI FVSVTNEHLIDMDHEASFPGAF 240       219 PILLMKASRNCSCKSDAEYGLYSIYGCGIFELKENDRI FVSVTNEHLIDMDHEASFPGAF 278 
Dd	
QY	241 LVG 243     279 LVG 281
Dd	
RESULT 4	
AAW27134	ID ID standard; protein; 281 AA.
XX	
AW27134;	
XX	
02-APR-1998	(first entry)
XX	

```

RESULT 5
AAW19787
ID AAW19787 standard; protein; 281 AA.
XX
AC AAW19787;
XX
DT 24-SEP-1997 (first entry)
XX
DE Human apoptosis inducer cytokine TRAIL.
XX
KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW thrombotic microangioplasty; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..118 /label= Cytoplasmic_domain
FT Domain 19..38 /label= Transmembrane_domain
FT Domain 39..281 /label= Extracellular_domain
FT /note= "contains a receptor-binding region"
FT Cleavage-site 89..90 /note= "potential KEX2 protease processing site"
FT Modified-site 109..111 /note= "potential N-glycosylation site"
FT Cleavage-site 149..150 /note= "potential KEX2 protease processing site"
XX
PN WO9701633-A1.
XX
PD 16-JAN-1997.
XX
PF 25-JUN-1996; 96WO-US010895.
XX
PR 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Wiley SR, Goodwin RG;
XX
DR N-PSDB; AAT72847.
XX
PT TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
PT cells - useful for treating thrombotic microangiopathy, cancer and viral
PT infection and for use in assays.
XX
PS Claim 10; Page 43-44; 62pp; English.
XX
CC Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
CC (AAW19787) is a novel cytokine that induces apoptosis of certain target
CC cells, including cancer cells and virally infected cells. Its amino acid
CC sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
CC polypeptides) can be expressed in host cells and used in the treatment of
CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
CC to raise antibodies that may be useful for treating thrombotic
CC microangiopathies
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.4e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEE 98

```

Query Match

100.0%; Score 1287; DB 2; Length 281;

CC	studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
CC	(e.g. to isolate antigens for vaccine development). The polypeptides can
CC	be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
CC	treatment of blood or bone-marrow), or to treat viral infections
XX	
SQ	Sequence 281 AA;
	Query Match 100.0%; Score 1287; DB 2; Length 281;
	Best Local Similarity 100.0%; Pred. No. 3.4e-117;
	Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 TNELKQMDDKYSGGIACFLKEDDSYWDNDEESMNSPCWVKWQLRLVRKMILTSEE 60 
Dd	39 TNELKQMDDKYSGGIACFLKEDDSYWDNDEESMNSPCWVKWQLRLVRKMILTSEE 98 
Qy	61 TISTVGEKQNISPLVREGRGPORVAHHITGTRSNLTSSPNKSNEKALGRKINSWEISSR 120 
Dd	99 TISTVGEKQNISPLVREGRGPORVAHHITGTRSNLTSSPNKSNEKALGRKINSWEISSR 158 
Qy	121 SGHSFSLNLHLRNGELVLIIHEKGFPYYIYSOTYFRFOBEIKENTKNDKOMVOYIYKYTSYPD 180 
Dd	159 SGHSFSLNLHLRNGELVLIIHEKGFPYYIYSOTYFRFOBEIKENTKNDKOMVOYIYKYTSYPD 218 

Qy	181	PILLMSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240
Db	219	PILLMSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278
Qy	241	LVG 243	
Db	279	LVG 281	
RESULT 8			
AAW44354			
ID	AAW44354	standard; protein; 281 AA.	
XX			
AC	AAW44354;		
XX			

DI	28-MAR-1998	(1118L entry)
XX		
DE	Human AGP-1.	
XX		
KW	Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;	
KW	bone resorption; haematopoietic disease.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9746686-A2.	
XX		
PD	11-DEC-1997.	
XX		
PF	06-JUN-1997; 97WO-US009895.	
XX		
PR	07-JUN-1996; 96US-00660562.	
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Johnson MJ, Simonet WS, Danilenko DM;	
XX		
DR	WPI; 1998-042194/04.	
DR	N-PSDB; AAV15295.	
XX		

Claim 7; Page 36-37; 54pp; English.

CC reagents for detecting AGP-1 expression. Nucleic acid complementary to  
 CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are  
 CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus  
 CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or  
 CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,  
 CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat  
 CC haematopoietic diseases associated with reduction in the number of bone  
 CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused  
 CC by disease, injury or exposure to myelosuppressive agents. Host cells,  
 CC transformed with expression vectors containing AGP-1 DNA, are used to  
 CC produce recombinant AGP-1  
 XX  
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-117;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60  
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98  
 QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
 DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
 QY 121 SGHSFLSNLHRLNGELVIEHKGFFYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYDP 180  
 DB 159 SGHSFLSNLHRLNGELVIEHKGFFYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYDP 218  
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAF 240  
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAF 278  
 QY 241 LVG 243  
 DB 279 LVG 281

RESULT 9  
 AAY01517  
 ID AAY01517 standard; peptide; 281 AA.

XX AC AAY01517;  
 XX DT 27-MAY-1999 (first entry)  
 XX Protein associated with neurodegenerative and autoimmune diseases.  
 XX DE Neurodegenerative disease; autoimmune disease; inflammatory disease;  
 XX KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;  
 XX KW surface receptor; TRAIL protein.

XX OS Homo sapiens.  
 XX PN FR2766713-A1.  
 XX PD 05-FEB-1999.  
 XX PF 04-AUG-1997; 97FR-00010176.  
 XX PR 04-AUG-1997; 97FR-00010176.  
 XX PA (INMR ) BIO MERIEUX.  
 XX PI Rieger F, Belliveau JF, Perron H;  
 XX DR WPI; 1999-156177/14.

XX Use of polypeptide derived from TRAIL protein for diagnosis of  
 PT degenerative disease - autoimmunity and inflammation, also useful in  
 PT prevention or treatment, and similar use of corresponding ligand and  
 PT nucleic acid.

XX Claim 2; Page 13; 21pp; French.

XX The specification describes the use a polypeptide corresponding to at  
 CC least the primary sequence of part of the present sequence to produce a  
 CC diagnostic, prophylactic or therapeutic composition useful in cases of  
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can  
 CC be used in treatment of neurodegenerative diseases, lupus erythematosus,  
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central  
 CC nervous system cells, antigenic and specifically recognise the surface and  
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and  
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an  
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific  
 CC receptors, inhibiting formation of natural complex

SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-117;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60  
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98  
 QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
 DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
 QY 121 SGHSFLSNLHRLNGELVIEHKGFFYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYDP 180  
 DB 159 SGHSFLSNLHRLNGELVIEHKGFFYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYDP 218  
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAF 240  
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAF 278  
 QY 241 LVG 243  
 DB 279 LVG 281

RESULT 10  
 AAY27012  
 ID AAY27012 standard; protein; 281 AA.

XX AC AAY27012;  
 XX DT 24-SEP-1999 (first entry)  
 XX Human Apo-2 ligand (Apo-2L) polypeptide.  
 XX DE Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;  
 XX KW lupus; immune-mediated glomerular nephritis; human.

XX OS Homo sapiens.  
 XX PN WO9936535-A1.  
 XX PD 22-JUL-1999.  
 XX PF 15-JAN-1999; 99WO-US001039.  
 XX PR 15-JAN-1998; 98US-00007886.  
 XX PR 15-APR-1998; 98US-00060533.  
 XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;  
 XX WPI; 1999-444397/37.  
 XX DR N-PSDB; AAX86987.



PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis  
 PT in mammalian cancer cells.  
 XX  
 XX Claim 1; Fig 1A; 86pp; English.

CC This sequence represents a novel human cytokine, designated Apo-2 ligand  
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant  
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer  
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to  
 CC induce apoptosis for pathological conditions characterized by decreased  
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-  
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid  
 CC coding sequence can also be used in quantitative and screening diagnostic  
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases  
 CC associated with increased apoptosis  
 XX  
 XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-117; Mismatches 0; Indels 0; Gaps 0;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEE 60  
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEE 98  
 QY 61 TISTVQEKQNI SPLVRERGPQVAHAITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
 DB 99 TISTVQEKQNI SPLVRERGPQVAHAITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
 QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKOMQYIYKTSYDP 180  
 DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKOMQYIYKTSYDP 218  
 QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
 DB 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
 QY 241 LVG 243  
 DB 279 LVG 281

RESULT 11  
 ID AAY81956  
 AC AAY81956;  
 DT 10-JUL-2000 (first entry)  
 DE Human Apo-2 ligand protein sequence.

XX Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;  
 XX therapy; apoptosis; cancer.  
 XX Homo sapiens.

XX US6046048-A.  
 XX 04-APR-2000.  
 XX 08-JAN-1997; 97US-00780496.  
 XX 09-JAN-1996; 96US-0009755P.  
 XX (GETH ) GENENTECH INC.

XX Kim KJ, Ashkenazi AJ, Chuntharapai A;  
 XX WPI; 2000-282690/24.  
 XX N-PSDB; AAA07425.

PT New isolated monoclonal antibodies having antigen specificity for Apo-2  
 PT ligand, e.g. 2E11 or 5C2, useful for detecting the expression of Apo  
 PT -2 ligand serum, and for treating diseases associated with increased  
 XX apoptosis.

XX Claim 9; Fig 1a; 46pp; English.

CC This sequence is the human Apo-2 ligand protein, which is recognised by  
 CC monoclonal antibodies produced by the hybridoma cell lines of the  
 CC invention. The hybridoma cell lines are deposited under the American Type  
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258  
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic  
 CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,  
 CC tissues, or serum. The antibodies may also be employed as therapeutics.  
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand  
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat  
 CC pathological conditions or diseases associated with increased apoptosis.  
 CC They are also useful for the affinity purification of Apo-2 ligand from  
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may  
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells

XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 3; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-117; Mismatches 0; Indels 0; Gaps 0;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEE 60  
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVKQLRQVRKMLRTSEE 98  
 QY 61 TISTVQEKQNI SPLVRERGPQVAHAITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
 DB 99 TISTVQEKQNI SPLVRERGPQVAHAITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
 QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKOMQYIYKTSYDP 180  
 DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKOMQYIYKTSYDP 218  
 QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
 DB 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
 QY 241 LVG 243  
 DB 279 LVG 281

RESULT 12  
 ID AAB24038  
 AC AAB24038;  
 DT 25-JAN-2001 (first entry)

XX Human PRO1096 protein sequence SEQ ID NO:51.

XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
 XX identification; tumourigenesis; anticancer; detection.

XX Homo sapiens.  
 XX WO200053750-A1.  
 XX 14-SEP-2000.

XX 02-DEC-1999; 99WO-US028551.  
 XX 08-MAR-1999; 99WO-US005028.  
 XX 01-SEP-1999; 99WO-US020111.  
 XX 23-OCT-1999; 99US-0162506P.  
 XX 30-NOV-1999; 99WO-US028313.

PR	01-DEC-1999;	99WO-US028634.	
XX	(GETH )	GENENTECH INC.	
PA	Botstein D,	Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;	
PI	WPI; 2000-594320/56.		
DR	N-PSDB; AAC58120.		
XX			
XX	Antibodies specific for PRO polypeptides, used to diagnose and inhibit		
PT	the growth of tumors in mammals, and to identify inhibitors of PRO		
PT	polypeptide activity or expression.		
XX			
PS	Claim 61; Fig 36; 226pp; English.		
XX			
CC	The present invention describes an antibody that binds to a human protein		
CC	(I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;		
CC	PRO1927; PRO3567; PRO1295; PRO1303; PRO1304; PRO4344; PRO4354; PRO4397;		
CC	PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer		
CC	activity and can be used to diagnose tumours in mammals, by detecting		
CC	complex formation when the antibody is contacted with test cells.		
CC	Increased expression of genes encoding (I) can also be detected to		
CC	diagnose tumours. Agents which inhibit the activity of (I), especially		
CC	the antibodies, or an antisense oligonucleotide which hybridises to genes		
CC	encoding (I), can be used to inhibit tumour growth, preferably by		
CC	identifying compounds which inhibit the biological activity of (I). AAC58019		
CC	to AAC58102 represent PCR primers and hybridisation probes used in		
CC	examples from the present invention for human PRO sequences. AAC58103 to		
CC	AAC58122 and AAC24021 to AAC24040 represent human PRO polynucleotide and		
CC	protein sequences given in the exemplification of the present invention		
XX			
SQ	Sequence 281 AA;		
Query Match 100.0%; Score 1287; DB 3; Length 281;			
Best Local Similarity 100.0%; Pred. No. 3.4e-117;			
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TNELQMOMDKYKSGIACFLKEDDSYWDNDDESMNSPCQVQKWQLVRKMLRTSEE	60
DB	39	TNELQMOMDKYKSGIACFLKEDDSYWDNDDESMNSPCQVQKWQLVRKMLRTSEE	98
QY	61	TISTVQEKQONISPLVRERGQORVAHIITGTRGSRNTLSSPNSKNEKALGRKINSWESSR	120
DB	99	TISTVQEKQONISPLVRERGQORVAHIITGTRGSRNTLSSPNSKNEKALGRKINSWESSR	158
QY	121	SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD	180
DB	159	SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD	218
QY	181	PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240
DB	219	PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278
QY	241	LVG 243	
DB	279	LVG 281	
RESULT 14			
AAB08545			
ID	AAB08545	standard; protein; 281 AA.	
XX			
AC	AAB08545;		
XX			
DT	20-DEC-2000	(first entry)	
XX			
XX	Amino acid sequence of a human TRAIL polypeptide.		
XX			
XX	Human; TRAIL; tumour necrosis factor; TNF, diterpenoid triepoxide;		
KW	TNF related apoptosis-inducing ligand; tumour cell;		
KW	TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;		
KW	non-small cell lung carcinoma.		

XX	Homo sapiens.		
OS	WO2000048619-A1.		
PN	24-AUG-2000.		
XX			
PD	15-FEB-2000; 2000WO-US003891.		
XX			
PF	16-FEB-1999; 99US-0120313P.		
XX			
PR	(STRD ) UNIV LELAND STANFORD JUNIOR.		
XX			
PA	Rosen GD;		
XX			
PI	WPI; 2000-558253/51.		
XX	N-PSDB; AAA64325.		
DR	Killing of tumor cells, e.g. solid tumors or carcinoma, comprises		
XX	administration of synergistic combination of diterpenoid diepoxide and		
PT	tumor necrosis factor related apoptosis-inducing ligand.		
PT			
XX	Disclosure; Page 23-24; 29pp; English.		
PS			
XX	The present sequence represents a human TRAIL (tumour necrosis factor		
CC	(TNF) related apoptosis-inducing ligand) polypeptide. The specification		
CC	describes a method for enhanced killing of tumour cells. The method		
CC	comprises contacting a susceptible tumour cell with a synergistic mixture		
CC	of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined		
CC	dosage to kill at least 50 % of the cells. This mixture is synergistic,		
CC	and so is active at lower doses and against otherwise resistant cell		
CC	lines. The method is used for killing tumour cells, especially solid		
CC	tumours or carcinomas (especially mammary carcinoma or non-small cell		
CC	lung carcinoma)		
XX			
SQ	Sequence 281 AA;		
Query Match 100.0%; Score 1287; DB 3; Length 281;			
Best Local Similarity 100.0%; Pred. No. 3.4e-117;			
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TNELQMOMDKYKSGIACFLKEDDSYWDNDDESMNSPCQVQKWQLVRKMLRTSEE	60
DB	39	TNELQMOMDKYKSGIACFLKEDDSYWDNDDESMNSPCQVQKWQLVRKMLRTSEE	98
QY	61	TISTVQEKQONISPLVRERGQORVAHIITGTRGSRNTLSSPNSKNEKALGRKINSWESSR	120
DB	99	TISTVQEKQONISPLVRERGQORVAHIITGTRGSRNTLSSPNSKNEKALGRKINSWESSR	158
QY	121	SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD	180
DB	159	SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPD	218
QY	181	PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240
DB	219	PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	278
QY	241	LVG 243	
DB	279	LVG 281	
RESULT 14			
AAB28691			
ID	AAB28691	standard; protein; 281 AA.	
XX			
AC	AAB28691;		
XX			
DT	14-FEB-2001	(first entry)	
XX			
DE	Human AGP-1.		
XX			
KW	Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;		

KW	antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW	human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW	hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW	transplant rejection; cardiovascular disease; arteriosclerosis.
XX	
OS	Homo sapiens.
XX	
PN	WO2000063253-A1.
XX	
PD	26-OCT-2000.
XX	
PF	24-MAR-2000; 2000WO-US008004.
XX	
PP	16-APR-1999; 99US-00293245.
XX	
PR	(AMGE-) AMGEN INC.
XX	
PA	Hsu H, Meng S;
XX	
PI	
XX	WPI; 2000-665240/64.
DR	N-PSDB; AAC67831.
DR	
XX	
PT	Fusion protein of AGP-1 protein and an Fc region, used to treat
PT	proliferative disorders, immune disorders, and virally-induced disorders.
XX	
PS	Claim 3; Fig'2; 93pp; English.
XX	
CC	The present sequence is human AGP-1, a type II transmembrane protein.
CC	Fusion proteins comprising an Fc immunoglobulin region fused to the N-
CC	terminal portion of the AGP-1 protein have been produced. The fusion
CC	proteins can be used to induce apoptosis in a tissue, and to treat
CC	proliferative disorders, immune disorders, or virally-induced disorders.
CC	The proliferative disorders include cancers, such as breast, prostate,
CC	lung or colon cancer. The viral infections include hepatitis, and
CC	acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC	be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC	such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC	proteins have increased biological activity compared to the soluble AGP-1
CC	proteins used in prior art therapies
XX	
SQ	Sequence 281 AA;
XX	

DT	21-MAR-2001	(first entry)
XX		
DE	Human PRO1096 protein.	
XX		
KW	Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;	
KW	antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;	
KW	PRO agonist; cancer; inflammatory disorder; immunological disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2000073348-A2.	
XX		
PD	07-DEC-2000.	
XX		
PF	30-MAY-2000; 2000WO-US014941.	
XX		
PR	02-JUN-1999; 99WO-US012252.	
PR	22-JUN-1999; 99US-0140650P.	
PR	23-JUN-1999; 99US-0141037P.	
PR	20-JUL-1999; 99US-0144758P.	
PR	01-SEP-1999; 99WO-US020111.	
PR	08-SEP-1999; 99WO-US020594.	
PR	29-OCT-1999; 99US-0162506P.	
PR	30-NOV-1999; 99WO-US028313.	
PR	01-DEC-1999; 99WO-US028634.	
PR	02-DEC-1999; 99WO-US028551.	
PR	09-DEC-1999; 99US-0170262P.	
PR	16-DEC-1999; 99WO-US030095.	
PR	20-DEC-1999; 99WO-US030399.	
PR	06-JAN-2000; 2000WO-US000376.	
PR	11-FEB-2000; 2000WO-US003565.	
PR	18-FEB-2000; 2000WO-US004341.	
PR	18-FEB-2000; 2000WO-US004342.	
PR	02-MAR-2000; 2000WO-US005841.	
PR	03-MAR-2000; 2000US-0187202P.	
PR	10-MAR-2000; 2000WO-US006319.	
PR	15-MAR-2000; 2000WO-US006884.	
PR	30-MAR-2000; 2000WO-US008439.	
PR	17-MAY-2000; 2000WO-US013705.	
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;	
PI	Shelton DL, Smith V, Watanabe CK, Wood WI;	
XX		
DR	WPI: 2001-016509/02.	
DR	N-PSDB; AAC91579.	
XX		
PT	Twenty eight nucleic acids encoding PRO polypeptides which are useful for	
PT	treating various tumors, e.g. breast cancer, and other inflammatory,	
PT	angiogenic and immunological disorders.	
XX		
PS	Claim 31; Fig 54; 188pp; English.	
XX		
CC	The present sequence is one of twenty eight novel PRO polypeptides. The	
CC	PRO polypeptides and their agonists, including antibodies, peptides, and	
CC	small molecule agonists, may be used to treat various tumors, e.g.,	
CC	cancers such as breast cancer, ovarian cancer, renal cancer, colorectal	
CC	cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,	
CC	central nervous system cancer, melanoma or leukaemia. They are also	
CC	useful for treating other disorders such as neuronal, glial, astrocytal.	
CC	hypothalamic and other glandular, macrophagal, epithelial, stromal and	
CC	biastocelic disorders, and inflammatory, angiogenic and immunological	
CC	disorders	
XX		
SQ	Sequence 281 AA;	
	Query Match 100.0%; Score 1287; DB 4; Length 281;	
	Best Local Similarity 100.0%; Pred. No. 3.4e-117;	
	Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 TNELKQMDKYSGKGIACFLKEDDSYDNPDEESMNSPCWQVKQLRQLRVKHLRTSEE 60	

Db	39	TNELKOMQDKYKSGIACFLKEDDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILFTSEE	98
Qy	61	TISTVOEKQONTISPLVREGRQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120
Db	99	TISTVOEKQONISPLVREGRQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	158
Qy	121	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD	180
Db	159	SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD	218
Qy	181	PILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF	240
Db	219	PILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF	278
Qy	241	LVG	243
Db	279	LVG	281

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Job time : 109.052 secs

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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:01:21 ; Search time 564.372 Seconds  
(without alignments)  
165.329 Million cell updates/sec

Title: US-10-662-429-2\_COPY\_39\_281

Perfect score: 1287

Sequence: 1 TWELKQMDKYSKGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	279	13	US-10-066-209-3
2	1287	100.0	281	8	US-08-916-625B-6
3	1287	100.0	281	8	US-08-971-317A-8
4	1287	100.0	281	9	US-09-813-329-17
5	1287	100.0	281	9	US-09-933-663-8
6	1287	100.0	281	9	US-09-934-465-1
7	1287	100.0	281	10	US-09-919-039-118
8	1287	100.0	281	13	US-10-011-125-4
9	1287	100.0	281	13	US-10-001-054-54
10	1287	100.0	281	14	US-10-093-766-54
11	1287	100.0	281	14	US-10-174-654-11

12	1287	100.0	281	14	US-10-151-882-41	Sequence 41, Appl
13	1287	100.0	281	14	US-10-218-547-20	Sequence 20, Appl
14	1287	100.0	281	14	US-10-322-673-72	Sequence 72, Appl
15	1287	100.0	281	14	US-10-139-785-66	Sequence 66, Appl
16	1287	100.0	281	14	US-10-310-793-26	Sequence 26, Appl
17	1287	100.0	281	15	US-10-279-687-8	Sequence 8, Appl
18	1287	100.0	281	15	US-10-292-486-5	Sequence 5, Appl
19	1287	100.0	281	15	US-10-333-712-1	Sequence 1, Appl
20	1287	100.0	281	15	US-10-662-429-2	Sequence 20, Appl
21	1287	100.0	281	15	US-10-202-062-20	Sequence 2, Appl
22	1287	100.0	281	15	US-10-662-430-2	Sequence 2, Appl
23	1287	100.0	281	15	US-10-662-431-2	Sequence 2, Appl
24	1287	100.0	281	15	US-10-652-244-2	Sequence 2, Appl
25	1287	100.0	281	15	US-10-381-160-5	Sequence 5, Appl
26	1287	100.0	281	16	US-10-755-889-210	Sequence 210, App
27	1287	100.0	281	16	US-10-491-326-1	Sequence 1, Appl
28	1287	100.0	281	16	US-10-810-063-2	Sequence 2, Appl
29	1287	100.0	281	16	US-10-825-282-22	Sequence 22, Appl
30	1287	100.0	281	16	US-10-825-282-24	Sequence 24, Appl
31	1287	100.0	281	16	US-10-393-116-5	Sequence 5, Appl
32	1287	100.0	281	16	US-10-688-845-36	Sequence 36, Appl
33	1287	100.0	281	16	US-10-861-685-1	Sequence 1, Appl
34	1287	100.0	281	17	US-10-771-254-1	Sequence 1, Appl
35	1287	100.0	281	17	US-10-855-559-2	Sequence 2, Appl
36	1287	100.0	281	17	US-10-451-200-5	Sequence 5, Appl
37	1287	100.0	281	17	US-10-495-353-1	Sequence 1, Appl
38	1287	100.0	281	17	US-10-652-979-1	Sequence 1, Appl
39	1282	99.6	266	16	US-10-738-423-10	Sequence 10, Appl
40	1265	98.3	279	16	US-10-367-094-22	Sequence 22, Appl
41	1246	96.8	283	17	US-10-978-203-23	Sequence 23, Appl
42	1246	96.8	283	17	US-10-978-131-23	Sequence 23, Appl
43	1078.5	83.8	246	9	US-09-855-544A-13	Sequence 13, Appl
44	1047	81.4	271	16	US-10-781-866-30	Sequence 30, Appl
45	997.5	77.5	400	16	US-10-723-003-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1

US-10-066-209-3  
; Sequence 3, Application US/10066209  
; Publication No. US2002015110A1  
; GENERAL INFORMATION:  
; APPLICANT: Brigham-Burke, Michael R.  
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND  
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2  
; FILE REFERENCE: CH-50030-D1  
; CURRENT APPLICATION NUMBER: US/10/066,209  
; PRIOR FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: 09/072,993  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/055,513  
; PRIOR FILING DATE: 1997-08-13  
; PRIOR APPLICATION NUMBER: 60/056,980  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/057,550  
; PRIOR FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 279  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-10-066-209-3

Query Match 100.0%; Score 1287; DB 13; Length 279;  
Best Local Similarity 100.0%; Pred. NO. 1e-110;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWELKQMDKYSKGIACFLKEDDSYWDNDESNMSPCWQVQWLRVLRKMLRTSEE 60  
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Db 37 TNELKQMDKYSGKIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLRTSBE 96  
QY 61 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
Db 97 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156  
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYD 180  
Db 157 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYD 216  
QY 181 PILLKMSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
Db 217 PILLKMSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276  
QY 241 LVG 243  
Db 277 LVG 279

## RESULT 2

US-08-916-625B-6  
; Sequence 6, Application US/08916625B  
; Publication No. US20010010924A1  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH C.  
; APPLICANT: YOUNG, PETER R.  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED  
; TITLE OF INVENTION: RECEPTOR, TR6  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,625B  
; FILING DATE: 22-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/853,684  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: 60/041,230  
; FILING DATE: 14-MARCH-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-S0008-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846189  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-916-625B-6

Query Match 100.0%; Score 1287; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1e-110;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TNELKQMDKYSGKIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLRTSBE 60  
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Db 39 TNELKQMDKYSGKIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLRTSBE 98  
QY 61 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
Db 99 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYD 180  
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYD 218  
QY 181 PILLKMSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
Db 219 PILLKMSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
QY 241 LVG 243  
Db 279 LVG 281

## RESULT 3

US-08-971-317A-8  
; Sequence 8, Application US/08971317A  
; Publication No. US20010010925A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/971,317A  
; FILING DATE: 17-NOV-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goller, Mimi C  
; REGISTRATION NUMBER: 39,046  
; REFERENCE/DOCKET NUMBER: 6255.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (847) 935-7550  
; TELEFAX: (847) 938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. US20010010925A1e  
US-08-971-317A-8

Query Match 100.0%; Score 1287; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1e-110;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TNELKQMDKYSGKIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLRTSBE 60  
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Db 39 TNELKQMDKYSGKIACFLKEDDSYWDPNDESMNSPCQVKWQRLQRLVRKMLRTSBE 98  
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QY 61 T1STVQEKQONTISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
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Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD 180  
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD 218  
Qy 181 PILLMKSARNCSWCKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
Db 219 PILLMKSARNCSWCKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
Qy 241 LVG 243  
Db 279 LVG 281

## RESULT 4

US-09-813-329-17  
; Sequence 17, Application US/09813329  
; Patent No. US20020012968A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole  
; FILE OF INVENTION: Variants Thereof  
; FILE REFERENCE: D0016.np  
; CURRENT APPLICATION NUMBER: US/09/813,329  
; CURRENT FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/190,816  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 281.  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-813-329-17

Query Match 100.0%; Score 1287; DB 9; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1e-110;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEE 60  
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEE 98  
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD 180  
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD 218  
Qy 181 PILLMKSARNCSWCKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
Db 219 PILLMKSARNCSWCKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
Qy 241 LVG 243  
Db 279 LVG 281

## RESULT 5

US-09-193-663-8  
; Sequence 8, Application US/09193663  
; Patent No. US20020055624A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF  
; FILE REFERENCE: 6255.US.02  
; CURRENT APPLICATION NUMBER: US/09/193,663  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/065,916

; EARLIER FILING DATE: 1997-11-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-193-663-8

Query Match 100.0%; Score 1287; DB 9; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1e-110;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEE 60  
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEE 98  
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD 180  
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD 218  
Qy 181 PILLMKSARNCSWCKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
Db 219 PILLMKSARNCSWCKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
Qy 241 LVG 243  
Db 279 LVG 281

## RESULT 6

US-09-934-465-1  
; Sequence 1, Application US/09934465  
; Patent No. US20020102233A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669.22US03  
; CURRENT APPLICATION NUMBER: US/09/934,465  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 08/584,031  
; PRIOR FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-934-465-1

Query Match 100.0%; Score 1287; DB 9; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1e-110;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEE 60  
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEE 98  
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD 180  
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYD 218  
Qy 181 PILLMKSARNCSWCKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
Db 219 PILLMKSARNCSWCKDAEYGLYSYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

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QY 241 LVG 243
Db 279 LVG 281

RESULT 7
US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaer, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118

Query Match 100.0%; Score 1287; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRQLVRKMLRTSEE 98
QY 61 T1STVQEKQONISPLVREGPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 T1STVQEKQONISPLVREGPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYD 180
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYD 218
QY 181 PILLKMSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 9
US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/096891
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096894
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100263
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: 60/100390

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRQLVRKMLRTSEE 98
QY 61 T1STVQEKQONISPLVREGPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 T1STVQEKQONISPLVREGPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYD 180
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYD 218
QY 181 PILLKMSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 8
US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4
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; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/101476  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/107783  
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; PRIOR APPLICATION NUMBER: 60/108849  
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; PRIOR FILING DATE: 2001-08-13  
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; PRIOR FILING DATE: 2001-08-28

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; PRIOR APPLICATION NUMBER: 09/946374  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: PCT/US98/18824  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: PCT/US99/00106  
; PRIOR FILING DATE: 1999-01-05  
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; PRIOR FILING DATE: 1999-03-08  
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; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: PCT/US99/20111  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
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; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
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; PRIOR FILING DATE: 2000-02-11  
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; PRIOR FILING DATE: 2000-05-22  
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; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/22031  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: PCT/US00/23522  
; PRIOR FILING DATE: 2000-08-23  
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; PRIOR FILING DATE: 2001-03-01  
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; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
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; PRIOR FILING DATE: 2001-06-29  
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; PRIOR FILING DATE: 2001-07-09  
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; PRIOR FILING DATE: 2001-08-29  
; NUMBER OF SEQ ID NOS: 91

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; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match      100.0%; Score 1287; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDSDYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDSDYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 T1STVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 T1STVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQEEIKENTKNDKQMVQYIYKTSYDP 180
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQEEIKENTKNDKQMVQYIYKTSYDP 218

QY 181 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
Db 279 LVG 281

RESULT 10
US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54
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Query Match      100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDSDYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDSDYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 T1STVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 T1STVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQEEIKENTKNDKQMVQYIYKTSYDP 180
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQEEIKENTKNDKQMVQYIYKTSYDP 218

QY 181 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
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QY 241 LVG 243
Db 279 LVG 281

RESULT 11
US-10-174-654-11
; Sequence 11, Application US/10174654
; Publication No. US20030044937A1
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Jones, David A
; APPLICANT: Mills, Cynthia J
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/174,654
; FILING DATE: 19-Jun-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11
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Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDSDYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDSDYWDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 T1STVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 T1STVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQEEIKENTKNDKQMVQYIYKTSYDP 180
Db 159 SGHSFLSNLHLRNGELVIHEKGFYIYSQTYFFQEEIKENTKNDKQMVQYIYKTSYDP 218

QY 181 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
Db 279 LVG 281
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Db 279 LVG 281

RESULT 12
US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151.882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-41

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 180
DB 159 SGHSFSLNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 218
QY 181 PILLMKSARNCSWSDAEYGLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEYGLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 14
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 180
DB 159 SGHSFSLNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 218
QY 181 PILLMKSARNCSWSDAEYGLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEYGLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 180
DB 159 SGHSFSLNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 218
QY 181 PILLMKSARNCSWSDAEYGLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEYGLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 180
DB 159 SGHSFSLNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 218
QY 181 PILLMKSARNCSWSDAEYGLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEYGLYSIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
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QY 241 LVG 243  
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Db 279 LVG 281

RESULT 15  
US-10-139-785-66  
; Sequence 66, Application US/10139785  
; Publication No. US20030190685A1  
; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
; FILE REFERENCE: PF550  
; CURRENT APPLICATION NUMBER: US/10/139,785  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 60/369,860  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/341,237  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/331,310  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/331,044  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/327,364  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/323,807  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/309,176  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/294,981  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 60/293,473  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-139-785-66

Query Match 100.0%; Score 1287; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1e-110;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRQLVRKMILRTSEE 60  
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRQLVRKMILRTSEE 98  
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
Db 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYD 180  
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYD 218  
QY 181 PILLMKSARNCSWKADEYGLYSIYOGGIFELKENDRI FVSVTNEHLIDMDHEADSFFGAF 240  
Db 219 PILLMKSARNCSWKADEYGLYSIYOGGIFELKENDRI FVSVTNEHLIDMDHEADSFFGAF 278  
QY 241 LVG 243  
|||  
Db 279 LVG 281

Search completed: June 22, 2005, 06:39:14  
Job time : 565.372 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2005, 05:57:23 ; Search time 27.8244 Seconds  
(without alignments)  
651.935 Million cell updates/sec

Title: US-10-662-429-2\_COPY\_39\_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSKGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1287	100.0	281	1	US-08-670-354-2
3	1287	100.0	281	3	US-08-584-031-1
4	1287	100.0	281	3	US-08-780-496-1
5	1287	100.0	281	3	US-08-883-086-10
6	1287	100.0	281	3	US-09-320-424-2
7	1287	100.0	281	3	US-09-333-593A-6
8	1287	100.0	281	4	US-09-157-864-11
9	1287	100.0	281	4	US-09-825-563-2
10	1287	100.0	281	4	US-09-919-039-118
11	1287	100.0	281	4	US-09-582-450-1
12	1287	100.0	281	4	US-09-934-465-1
13	1287	100.0	281	4	US-10-011-125A-4
14	1287	100.0	281	5	PCT-US96-10895-2
15	1047	81.4	271	4	US-09-569-611C-30
16	988	76.8	253	3	US-09-320-424-11
17	988	76.8	253	4	US-09-825-563-11
18	988	76.8	256	3	US-09-320-424-13
19	988	76.8	256	4	US-09-825-563-13
20	930	72.3	177	3	US-09-105-343A-7
21	863	67.1	291	1	US-08-670-354-6
22	863	67.1	291	3	US-09-320-424-6
23	863	67.1	291	5	PCT-US96-10895-6
24	863	67.1	291	5	PCT-US96-10895-6
25	850	66.0	161	4	US-09-565-423-7
26	504	50.8	183	3	US-09-105-343A-8
27	544	42.3	169	4	US-09-569-611C-29

28	446	34.7	85	4	US-09-632-287A-12	Sequence 12, Appl
29	425	33.0	121	4	US-09-513-999C-7833	Sequence 7833 Ap
30	292	22.7	120	4	US-09-569-611C-32	Sequence 32, Appl
31	291	22.6	101	1	US-08-670-354-4	Sequence 4, Appl
32	291	22.6	101	3	US-09-320-424-4	Sequence 4, Appl
33	291	22.6	101	4	US-09-825-563-4	Sequence 4, Appl
34	291	22.6	101	5	PCT-US96-10895-4	Sequence 4, Appl
35	291	22.6	122	4	US-09-569-611C-31	Sequence 31, Appl
36	245.5	19.1	87	4	US-09-632-287A-13	Sequence 13, Appl
37	238.5	18.5	294	3	US-08-996-139-11	Sequence 11, Appl
38	238.5	18.5	294	3	US-08-995-659-11	Sequence 11, Appl
39	238.5	18.5	294	3	US-09-215-649A-11	Sequence 11, Appl
40	238.5	18.5	294	4	US-09-577-780-11	Sequence 11, Appl
41	238.5	18.5	294	4	US-09-577-800-11	Sequence 11, Appl
42	238.5	18.5	294	4	US-09-466-496-11	Sequence 11, Appl
43	238.5	18.5	294	4	US-09-871-856-11	Sequence 11, Appl
44	238.5	18.5	294	4	US-09-871-291-11	Sequence 11, Appl
45	238.5	18.5	294	4	US-09-877-650-11	Sequence 11, Appl

## ALIGNMENTS

## RESULT 1

US-09-072-993C-3  
; Sequence 3, Application US/09072993C  
; Patent No. 6346388  
; GENERAL INFORMATION:  
; APPLICANT: Michael R. Brigham-Burke  
; APPLICANT: Peter R. Young  
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND  
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2  
; FILE REFERENCE: GH-50030  
; CURRENT APPLICATION NUMBER: US/09/072,993C  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/055,513  
; PRIOR FILING DATE: 1997-08-13  
; PRIOR APPLICATION NUMBER: 60/056,980  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/057,550  
; PRIOR FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 279  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-072-993C-3

Query Match	100.0%;	Score 1287;	DB 3;	Length 279;
Best Local Similarity	100.0%;	Pred. No. 2.8e-125;		
Matches 243;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TNELKQMDKYSKGIACFLKDDSYWDPNDEBSMNSPCWQVKWLQRLVKMLRTSEE	60	
Db	37	TNELKQMDKYSKGIACFLKDDSYWDPNDEBSMNSPCWQVKWLQRLVKMLRTSEE	96	
Qy	61	TISTVQEKQONISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSMESSR	120	
Db	97	TISTVQEKQONISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSMESSR	156	
Qy	121	SGHSFLSNLHRLNGELVHKEGPPYIYSQTYFRQBEIKENTKNDKQVQIYKYTSYDP	180	
Db	157	SGHSFLSNLHRLNGELVHKEGPPYIYSQTYFRQBEIKENTKNDKQVQIYKYTSYDP	216	
Qy	181	PILLMSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	240	
Db	217	PILLMSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF	276	
Qy	241	LVG 243		
Db	277	LVG 279		

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RESULT 3
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Aeshkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match      100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKOMQDKYSGKGIACFLKEDDSYWDPNDESMNSPCQVKWQLVRKMLRTSEE 60
DB 39 TNELKOMQDKYSGKGIACFLKEDDSYWDPNDESMNSPCQVKWQLVRKMLRTSEE 98
QY 61 TISTVQEKQNTSPLVRESGPQVAAHITCTGRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNTSPLVRESGPQVAAHITCTGRGNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFQBEIKENTKDKQMVOYIYKITSYD 180
DB 159 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFQBEIKENTKDKQMVOYIYKITSYD 218
QY 181 PILMKASRNSCSWDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPF 240
DB 219 PILMKASRNSCSWDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASPF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 4
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: AVI Aeshkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: APO-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1

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; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5416  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-780-496-1

Query Match 100.0%; Score 1287; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-125;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQVVKMLRTSEE 60  
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQVVKMLRTSEE 98  
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKOMVOYIYKTSYDP 180  
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKOMVOYIYKTSYDP 218  
QY 181 PILLMSARNSCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
DB 219 PILLMSARNSCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
QY 241 LVG 243  
DB 279 LVG 281

RESULT 5  
US-08-883-086-10  
; Sequence 10, Application US/08883086  
; Patent No. 6171787  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, STEVEN  
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/883,086  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Porembski, Priscilla E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 6134, US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-937-0378  
; TELEFAX: 847-938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6171787e  
US-08-883-086-10

Query Match 100.0%; Score 1287; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-125;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQVVKMLRTSEE 60  
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQVVKMLRTSEE 98  
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKOMVOYIYKTSYDP 180  
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKOMVOYIYKTSYDP 218  
QY 181 PILLMSARNSCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
DB 219 PILLMSARNSCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
QY 241 LVG 243  
DB 279 LVG 281

RESULT 6  
US-09-320-424-2  
; Sequence 2, Application US/09320424  
; Patent No. 6284236  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; APPLICANT: Goodwin, Raymond G.  
; TITLE OF INVENTION: Cytokine that Induces Apoptosis  
; FILE REFERENCE: 2835-E  
; CURRENT APPLICATION NUMBER: US/09/320,424  
; CURRENT FILING DATE: 1999-05-26  
; EARLIER APPLICATION NUMBER: 09/190,046  
; EARLIER FILING DATE: 1998-11-10  
; EARLIER APPLICATION NUMBER: 09/048,641  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 08/670,354  
; EARLIER FILING DATE: 1996-06-25  
; EARLIER APPLICATION NUMBER: 08/548,368  
; EARLIER FILING DATE: 1995-11-01  
; EARLIER APPLICATION NUMBER: 08/496,632  
; EARLIER FILING DATE: 1995-06-29  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: human  
US-09-320-424-2

Query Match 100.0%; Score 1287; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-125;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQVVKMLRTSEE 60  
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQVVKMLRTSEE 98  
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMWQYIYKYTSYD 180  
|||  
Db 159 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMWQYIYKYTSYD 218  
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
|||  
Db 219 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
QY 241 LVG 243  
|||  
Db 279 LVG 281

## RESULT 7

US-09-333-593A-6  
; Sequence 6, Application US/09333593A  
; Patent No. 6313269  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH C.  
; APPLICANT: YOUNG, PETER R.  
; APPLICANT: MARSHALL, LISA A.  
; APPLICANT: KOSHAK, AMY K.  
; APPLICANT: TAN, KONG B.  
; APPLICANT: TRUNEH, ALEMSEGED  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,  
; FILE REFERENCE: GH-50008-2  
; CURRENT APPLICATION NUMBER: US/09/333,593A  
; CURRENT FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 08/916,625  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 08/853,684  
; PRIOR FILING DATE: 1997-05-09  
; PRIOR APPLICATION NUMBER: 60/041,230  
; PRIOR FILING DATE: 1997-03-14  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-333-593A-6

Query Match 100.0%; Score 1287; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-125;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELQMOKDKYSKGIACFLKEDDSYWDPNDESMNSPCQVKWQLRQLVRKMLTSEE 60  
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Db 39 TNELQMOKDKYSKGIACFLKEDDSYWDPNDESMNSPCQVKWQLRQLVRKMLTSEE 98  
QY 61 TISTVOEQKQNTISPLVRERGQORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
|||  
Db 99 TISTVOEQKQNTISPLVRERGQORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
QY 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMWQYIYKYTSYD 180  
|||  
Db 159 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMWQYIYKYTSYD 218  
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
|||  
Db 219 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
QY 241 LVG 243  
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Db 279 LVG 281

## RESULT 8

US-09-157-864-11  
; Sequence 11, Application US/09157864  
; Patent No. 6440694

; GENERAL INFORMATION:  
; APPLICANT: Bienkowski, Michael J  
; APPLICANT: Mills, Cynthia J  
; APPLICANT: Jones, David A  
; TITLE OF INVENTION: TNP-Related Death Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property  
; ADDRESSEE: Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/157,864  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerber, Lori L.  
; REGISTRATION NUMBER: 41,113  
; REFERENCE/DOCKET NUMBER: 6111.N CNI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616/833-0974  
; TELEFAX: 616/833-8897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-157-864-11

Query Match 100.0%; Score 1287; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-125;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELQMOKDKYSKGIACFLKEDDSYWDPNDESMNSPCQVKWQLRQLVRKMLTSEE 60  
|||  
Db 39 TNELQMOKDKYSKGIACFLKEDDSYWDPNDESMNSPCQVKWQLRQLVRKMLTSEE 98  
QY 61 TISTVOEQKQNTISPLVRERGQORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120  
|||  
Db 99 TISTVOEQKQNTISPLVRERGQORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158  
QY 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMWQYIYKYTSYD 180  
|||  
Db 159 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQMWQYIYKYTSYD 218  
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240  
|||  
Db 219 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278  
QY 241 LVG 243  
|||  
Db 279 LVG 281

## RESULT 9

US-09-825-563-2  
; Sequence 2, Application US/09825563  
; Patent No. 6521228  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; APPLICANT: Goodwin, Raymond G.  
; TITLE OF INVENTION: Cytokine that Induces Apoptosis



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; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-825-563-2

Query Match          100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDQKYSKSGIACFLKEDDSYDNDDEESMNSPCQVKKQLRQLVKRMILRTSEE 60
   |||||
Db 39 TNELKQMDQKYSKSGIACFLKEDDSYDNDDEESMNSPCQVKKQLRQLVKRMILRTSEE 98
   |||||

QY 61 TISTVQEKQNISPLVRERGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
   |||||
Db 99 TISTVQEKQNISPLVRERGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
   |||||

QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPD 180
   |||||
Db 159 SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPD 218
   |||||

QY 181 PILLMKARNCSWSKDAEYGLYSIQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
   |||||
Db 219 PILLMKARNCSWSKDAEYGLYSIQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
   |||||

QY 241 LVG 243
   |||
Db 279 LVG 281

RESULT 10
US-09-919-039-118
; Sequence 118, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1
US-09-919-039-118

Query Match          100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;

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RESULT 12
US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. 6746668
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match      100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMILRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNLHLRNGELVIEHKGFFYYISQTYFRFQSEIKENTKNDKQMVQYIYKYTSYD 180
DB 159 SGHSFSLNLHLRNGELVIEHKGFFYYISQTYFRFQSEIKENTKNDKQMVQYIYKYTSYD 218
QY 181 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 13
US-10-011-125A-4
; Sequence 4, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125A-4

Query Match      100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMILRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNLHLRNGELVIEHKGFFYYISQTYFRFQSEIKENTKNDKQMVQYIYKYTSYD 180
DB 159 SGHSFSLNLHLRNGELVIEHKGFFYYISQTYFRFQSEIKENTKNDKQMVQYIYKYTSYD 218
QY 181 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 14
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match      100.0%; Score 1287; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMILRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCQVKWQRLQRLVRKMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
```

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Db      99 TISTVQEKQONISPLVRERGPQVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 158
Qy      121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPD 180
Db      159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPD 218
Qy      181 PILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db      219 PILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy      241 LVG 243
Db      279 LVG 281
```

## RESULT 15

```
US-09-569-611C-30
; Sequence 30, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-30
```

Query Match 81.4%; Score 1047; DB 4; Length 271;

Best Local Similarity 83.1%; Pred. No. 2.2e-100;

Matches 202; Conservative 2; Mismatches 5; Indels 34; Gaps 2;

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Qy      1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVQWLRLVRLKMLRTSEE 60
Db      63 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVQWLRLVRLK----- 114
Qy      61 TISTVQEKQONISPLVRERGPQVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db      115 -----KSNKIFLPLVRERGPQVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 168
Qy      121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPD 180
Db      169 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPD 228
Qy      181 PILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db      229 PILLMKSARNCSKDAEYGLYSIYOG-----IDMDHEASFFGAF 268
Qy      241 LVG 243
Db      269 LVG 271
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Search completed: June 22, 2005, 06:02:16

Job time : 28.8244 secs

**This page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2005, 06:19:02 ; Search time 40 Seconds  
(without alignments)  
675.923 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVGGPSLGTCVLIV.....NEHLIDMDHEASFGAPLVG 281

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries.

Database :

1: PIR.79.\*  
2: PIR.2.\*  
3: PIR.3.\*  
4: PIR.4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	2.8	643	2 G75599	probable drug tran
2	8	2.8	950	2 T09076	hypothetical prote
3	7	2.5	51	2 S63590	insulin - duckbill
4	7	2.5	93	2 F84175	hypothetical prote
5	7	2.5	96	2 F80423	H4 protein - Toxop
6	7	2.5	107	2 C90304	hypothetical prote
7	7	2.5	155	2 G72548	hypothetical prote
8	7	2.5	240	2 A39016	T-cell surface gly
9	7	2.5	247	2 D90053	hypothetical prote
10	7	2.5	251	2 T40807	hypothetical prote
11	7	2.5	263	2 T38003	hypothetical ser-t
12	7	2.5	327	2 H82736	hypothetical prote
13	7	2.5	329	2 D71887	ADFGlyceromanno-he
14	7	2.5	354	2 G71465	hypothetical prote
15	7	2.5	354	2 A81728	conserved hypotet
16	7	2.5	401	2 C82660	conserved hypotet
17	7	2.5	404	2 G90210	hypothetical prote
18	7	2.5	420	2 S53916	SUN4 protein precu
19	7	2.5	424	2 H84806	hypothetical prote
20	7	2.5	427	2 G71272	iron-sulfur cofact
21	7	2.5	428	2 B84192	zinc metalloprotei
22	7	2.5	429	2 B72109	GMP synthase CP059
23	7	2.5	429	2 C86512	GMP synthase [limp
24	7	2.5	442	2 AF2539	manganese transpor
25	7	2.5	475	2 T39359	probable udp-n-ace
26	7	2.5	511	2 T19496	hypothetical prote
27	7	2.5	554	2 A47503	epoxide hydrolase
28	7	2.5	565	2 C82280	sensor kinase cita
29	7	2.5	710	2 T22360	hypothetical prote

30	7	2.5	801	2 AE3032	conserved hypotet
31	7	2.5	801	2 G98253	hypothetical prote
32	7	2.5	809	2 T20430	hypothetical prote
33	7	2.5	913	2 D90183	ATP-dependent heli
34	7	2.5	926	2 T15683	hypothetical prote
35	7	2.5	979	2 JH0109	glycoprotein 14 pr
36	7	2.5	982	2 E88465	protein B0244.6 fi
37	7	2.5	1014	2 T36031	exonuclease ABC c
38	7	2.5	1377	2 T19214	UDP-glucose-glycop
39	7	2.5	1414	2 T33236	hypothetical prote
40	7	2.5	1847	2 E64477	replication factor
41	7	2.5	1891	2 T43262	calcium channel al
42	7	2.5	1975	2 B81192	hemagglutinin/hemo
43	7	2.5	1995	2 G81044	hemagglutinin/hemo
44	7	2.5	2015	2 B81989	hypothetical prote
45	7	2.5	3434	1 GNVVMV	genome polyprotein
46	6	2.1	47	2 T04365	ethylene responsiv
47	6	2.1	48	2 S78202	H+-transporting tw
48	6	2.1	55	2 AF2105	hypothetical prote
49	6	2.1	56	2 C60157	hypothetical prote
50	6	2.1	62	2 C97621	hypothetical prote
51	6	2.1	64	2 AG0025	probable bacteriof
52	6	2.1	65	2 AC0774	hypothetical prote
53	6	2.1	85	2 C91249	hypothetical prote
54	6	2.1	89	2 S78744	protein YDR363w-a
55	6	2.1	96	2 B82311	conserved hypotet
56	6	2.1	96	2 AE3205	transposase tnp [i
57	6	2.1	98	2 G91248	hypothetical prote
58	6	2.1	102	2 C95337	probable cytochrom
59	6	2.1	104	2 E69832	conserved hypotet
60	6	2.1	105	2 B86818	hypothetical prote
61	6	2.1	107	2 S09964	ig kappa chain V-J
62	6	2.1	107	2 A44887	glucose transpor
63	6	2.1	109	2 F84012	hypothetical prote
64	6	2.1	112	2 AC2887	conserved hypotet
65	6	2.1	112	2 H97662	hypothetical prote
66	6	2.1	115	2 B25924	ig kappa chain pre
67	6	2.1	116	2 C83166	probable chaperone
68	6	2.1	117	2 F97174	hypothetical prote
69	6	2.1	119	2 JQ2032	lambda 208 protein
70	6	2.1	122	2 D89803	conserved hypotet
71	6	2.1	128	2 AH0043	probable lipoprote
72	6	2.1	130	2 D64559	hypothetical prote
73	6	2.1	132	2 F86829	ribose ABC transpo
74	6	2.1	132	2 F70650	hypothetical prote
75	6	2.1	134	2 AC0855	probable regulator
76	6	2.1	135	2 B91078	transcription regu
77	6	2.1	135	2 T44999	hypothetical prote
78	6	2.1	137	2 S74888	hypothetical prote
79	6	2.1	137	2 D86944	conserved hypotet
80	6	2.1	137	2 T30095	hypothetical prote
81	6	2.1	137	2 F89954	conserved hypotet
82	6	2.1	143	1 WMB56H	transcription regu
83	6	2.1	143	2 T43976	transactivator lim
84	6	2.1	143	2 B71372	conserved hypotet
85	6	2.1	145	2 AC0053	DNA-directed DNA p
86	6	2.1	146	2 C85923	probable regulator
87	6	2.1	149	2 H70581	hypothetical prote
88	6	2.1	151	2 A75297	hypothetical prote
89	6	2.1	152	2 B64485	hypothetical prote
90	6	2.1	152	2 T43088	traj protein homol
91	6	2.1	154	2 F90546	deoxycytidylate de
92	6	2.1	157	2 A84402	hypothetical prote
93	6	2.1	161	2 H87183	integral membrane
94	6	2.1	162	2 T50253	Vacuolar ATP synth
95	6	2.1	165	2 S62563	adaptin complex sm
96	6	2.1	166	2 A75426	hypothetical prote
97	6	2.1	167	2 G95335	hypothetical prote
98	6	2.1	169	2 D72765	hypothetical prote
99	6	2.1	169	2 T31484	hypothetical prote
100	6	2.1	170	2 T48974	hypothetical prote

## ALIGNMENTS

## RESULT 1

G75599  
probable drug transport protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: G75599  
R:White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: G75599  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-643 <WHI>  
A:Cross-references: UNIPROT:Q9RZ93; GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF1225  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DRA0061  
A:Map position: 2

Query Match 2.8%; Score 8; DB 2; Length 643;  
Best Local Similarity 100.0%; Pred. No. 6.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLIVIFTV 24  
|||||

DB 231 VLIVIFTV 238

## RESULT 2

T09076  
hypothetical protein CGI (strain HB3) - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: T09076  
R:Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellem, T.E.  
Cell 91, 593-603, 1997

A:Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant  
A:Reference number: Z16556; MUID:98054002; PMID:9393853

A:Accession: T09076  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-950 <SUX>  
A:Cross-references: UNIPROT:O15788; EMBL:AF030690; NID:g2642510; PIDN:AAC47851.1; PID:g2  
C:Genetics:  
A:Gene: cgi

Query Match 2.8%; Score 8; DB 2; Length 950;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140  
|||||

DB 361 SNTLSSPN 368

## RESULT 3

S63590  
insulin - duckbill platypus  
C:Species: Ornithorhynchus anatinus (duckbill platypus)  
C:Date: 19-Mar-1997 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: S63590  
R:Nourse, A.; Treacy, G.B.; Shaw, D.C.; Jeffrey, P.D.  
Biol. Chem. Hopps-Seyler 377, 147-153, 1996

A:Title: Platypus insulin: indications from the amino acid sequence of significant differ  
A:Reference number: S63590; MUID:97021710; PMID:8868070

A:Accession: S63591  
A:Molecule type: protein

A:Residues: 1-30 <NOU2>  
A:Cross-references: UNIPROT:Q9TQV7  
A:Accession: S63590  
A:Molecule type: protein  
A:Residues: 31-51 <NOUI>  
C:Superfamily: insulin  
C:Keywords: hormone; pancreas  
F:1-30/31-51/Product: insulin #status experimental <MAT>  
F:1-30/Domain: insulin chain B #status experimental <BCH>  
F:31-51/Domain: insulin chain A #status experimental <ACH>  
F:7-37,19-50,36-41/Dissulfide bonds: #status predicted

Query Match 2.5%; Score 7; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 EKGFFYYI 184  
|||||

DB 21 EKGFFYYI 27

## RESULT 4

F84175  
hypothetical protein Vng0151c [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: F84175

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;  
Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Jung, K.H.; Alam, M.; Freitae, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lia  
A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: F84175  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-93 <STO>  
A:Cross-references: UNIPROT:Q9HSN3; GB:AE004437; NID:g10579798; PIDN:AAG18770.1; GSPDB:G  
C:Genetics:  
A:Gene: VNG0151C

Query Match 2.5%; Score 7; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 FVSVTNE 263  
|||||

DB 13 FVSVTNE 19

## RESULT 5

PS0423  
H4 protein - Toxoplasma gondii (fragment)

N:Alternate names: diagnostic antigen H4  
C:Species: Toxoplasma gondii

C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 09-Jul-2004  
C:Accession: PS0423

R:Johnson, A.M.; Iilana, S.

Gene 99, 127-132, 1991

A:Title: Cloning of Toxoplasma gondii gene fragments encoding diagnostic antigens.

A:Reference number: PS0423; MUID:91216437; PMID:2022319

A:Accession: PS0423

A:Molecule type: mRNA

A:Residues: 1-96 <JOH>

A:Cross-references: UNIPROT:Q27001; GB:M57302; NID:g161914; PID:g161915

C:Genetics:  
A:Gene: H4

Query Match 2.5%; Score 7; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FOREIKE 198  
 |||||  
 Db 2 FOREIKE 8

## RESULT 6

C90304  
 hypothetical protein SS01462 [imported] - Sulfolobus solfataricus  
 C;Species: Sulfolobus solfataricus  
 C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
 C;Accession: C90304  
 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
 arrett, R.A.; Ragan, M.A.; Senen, C.W.; Van der Oost, J.  
 submitted to GenBank, April 2001  
 A;Description: Sulfolobus solfataricus complete genome.  
 A;Reference number: A99139  
 A;Accession: C90304  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-107 <KUR>  
 A;Cross-references: UNIPROT:Q97Y77; GB:A5006641; NID:G13814690; PIDN:AAK41690.1; GSPDB:G  
 C;Genetics:  
 A;Gene: SS01462

Query Match 2.5%; Score 7; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 FFGAFLV 280  
 |||||  
 Db 46 FFGAFLV 52

## RESULT 7

G72548  
 hypothetical protein APE1675 - Aeropyrum pernix (strain K1)  
 C;Species: Aeropyrum pernix  
 C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
 C;Accession: G72548  
 R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah  
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K  
 DNA Res. 6, 83-101, 1999  
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr  
 A;Reference number: A72450; MUID:99310339; PMID:10382966  
 A;Accession: G72548  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-155 <KAW>  
 A;Cross-references: UNIPROT:Q9YBC2; DDBJ:AP000062; NID:G5105244; PIDN:BAAB0676.1; PID:di  
 A;Experimental source: strain K1  
 C;Genetics:  
 A;Gene: APE1675

Query Match 2.5%; Score 7; DB 2; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 TLSSPNS 141  
 |||||  
 Db 88 TLSSPNS 94

## RESULT 8

A39016  
 T-cell surface glycoprotein CD7 precursor - human  
 N;Alternate names: T-cell leukemia antigen  
 C;Species: Homo sapiens (man)  
 C;Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 09-Jul-2004  
 C;Accession: A39016; S03520  
 R;Schanberg, L.E.; Fleenor, D.E.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 603-607, 1991  
 A;Title: Isolation and characterization of the genomic human CD7 gene: structural simila

A;Reference number: A39016; MUID:91110576; PMID:1703303  
 A;Accession: A39016  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-240 <SCH>  
 A;Cross-references: UNIPROT:P09564; GB:M37271; NID:G180163; PIDN:AAA51953.1; PID:G180164  
 R;Aruffo, A.; Seed, B.  
 EMBO J. 6, 3313-3316, 1987

A;Title: Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell expr  
 A;Reference number: S03520; MUID:88111517; PMID:3501369  
 A;Accession: S03520  
 A;Molecule type: mRNA  
 A;Residues: 1-240 <ARU>  
 A;Cross-references: EMBL:X06180; NID:G29819; PIDN:CAA29546.1; PID:G732757

C;Genetics:  
 A;Gene: GDB:CD7  
 A;Cross-references: GDB:I19770; OMIM:186820  
 A;Map position: 17q25.2-17q25.3  
 A;Introns: 28/1  
 C;Keywords: glycoprotein; membrane protein; surface antigen; tandem repeat  
 F;1-25/Domain: signal sequence #status predicted <SIG>  
 F;26-240/Product: T-cell surface glycoprotein CD7 #status predicted <MAT>  
 F;145-180/Region: 9-residue repeats (X-P-X-A-S-A-L-P)

Query Match 2.5%; Score 7; DB 2; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 NTLSSPN 140  
 |||||  
 Db 231 NTLSSPN 237

## RESULT 9

D90053  
 hypothetical protein sarH2 [imported] - Staphylococcus aureus (strain N315)  
 C;Species: Staphylococcus aureus  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C;Accession: D90053  
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaifo, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146  
 A;Accession: D90053  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-247 <KUR>  
 A;Cross-references: UNIPROT:Q99RD5; GB:BA000018; PID:G13702449; PIDN:BAAB43590.1; GSPDB:G  
 A;Experimental source: strain N315  
 C;Genetics:  
 A;Gene: sarH2

Query Match 2.5%; Score 7; DB 2; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261  
 |||||  
 Db 91 RIFVSVT 97

## RESULT 10

T40807  
 hypothetical protein SPBP87.13 - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C;Accession: T40807  
 R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, October 1998  
 A;Reference number: Z21949  
 A;Accession: T40807

A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-251 <REC>  
 A:Cross-references: UNIPROT:O94262; EMBL:AL032684; PIDN:CAA21798.1; GSPDB:GN00067; SPDB:  
 A:Experimental source: strain 972h-; clone pl p8B7  
 C:Genetics:  
 A:Gene: SPDB:SPBP8B7.13  
 A:Map position: 2  
 A:Introns: 54/1  
 C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBP8B7.13

Query Match 2.5%; Score 7; DB 2; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DPNDDES 72  
 |||||  
 DB 73 DPNDDES 79

## RESULT 11

T38003  
 hypothetical ser-thr rich protein - fission yeast (Schizosaccharomyces pombe) (fragment)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 03-Nov-2000  
 C:Accession: T38003  
 R:Oliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, June 1997  
 A:Reference number: Z21760  
 A:Accession: T38003  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-263 <OLI>  
 A:Cross-references: EMBL:Z97209; PIDN:CAB10128.1; GSPDB:GN00066; SPDB:SPAC19G12.16C  
 A:Experimental source: strain 972h-; cosmid c19G12  
 C:Genetics:  
 A:Gene: SPAC23A1.01c; SPDB:SPAC19G12.16C  
 A:Map position: 1  
 C:Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase

Query Match 2.5%; Score 7; DB 2; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 EETISTV 103  
 |||||  
 DB 177 EETISTV 183

## RESULT 12

H82736  
 hypothetical protein XP0992 [imported] - Xylella fastidiosa (strain 985C)  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: H82736  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; MUID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: H82736  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-327 <SIM>  
 A:Cross-references: UNIPROT:QPPENG; GB:AE003937; GB:AE003849; NID:g9105920; PIDN:AAF8380  
 A:Experimental source: strain 985C  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh  
 -chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.;  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki  
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira  
 M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XF0992

Query Match 2.5%; Score 7; DB 2; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117  
 |||||  
 DB 164 SPLVRER 170

## RESULT 13

D71887  
 ADPglyceromanno-heptose 6-epimerase (EC 5.1.3.20) gmhd homolog [similarity] - Helicobacte  
 C:Species: Helicobacter pylori  
 A:Variety: strain J99  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 C:Accession: D71887  
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J  
 Nature 397, 176-180, 1999  
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
 A:Reference number: A71800; MUID:99120557; PMID:9923682  
 A:Accession: D71887  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-329 <ARN>  
 A:Cross-references: UNIPROT:Q9ZKY9; GB:AE001509; GB:AE001439; NID:g4155350; PIDN:AAD0636;  
 A:Experimental source: strain J99  
 C:Genetics:  
 A:Gene: gmhd  
 C:Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology  
 C:Keywords: isomerase

Query Match 2.5%; Score 7; DB 2; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNTLSS 138  
 |||||  
 DB 46 RSNTLSS 52

## RESULT 14

G71465  
 hypothetical protein CT839 - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
 C:Species: Chlamydia trachomatis  
 C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
 C:Accession: G71465  
 R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,  
 Science 282, 754-759, 1998  
 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract  
 A:Reference number: A71570; MUID:99000809; PMID:9784136  
 A:Accession: G71465  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-354 <ARN>  
 A:Cross-references: UNIPROT:O84846; GB:AE001356; GB:AE001273; NID:g33329299; PIDN:AAC6843;  
 A:Experimental source: serotype D, strain UW-3/Cx  
 C:Genetics:  
 A:Gene: CT839

Query Match 2.5%; Score 7; DB 2; Length 354;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 251 KENDRIF 257  
Db 150 KENDRIF 156

## RESULT 15

A81728  
Conserved hypothetical protein TC0227 [imported] - Chlamydia muridarum (strain Nigg)  
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: A81728  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Ginn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salberg, Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255; PMID:10684935  
A:Accession: A81728  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-354 <TET>  
A:Cross-references: UNIPROT:Q9PL80; GB:AE002289; GB:AE002160; NID:97190254; PIDN:AAF3909  
A:Experimental source: strain Nigg (MoPn)  
C:Genetics:  
A:Gene: TC0227

Query Match 2.5%; Score 7; DB 2; Length 354;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257  
Db 150 KENDRIF 156

## RESULT 16

C82660  
Conserved hypothetical protein XF1611 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: C82660  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing 405, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: C82660  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-401 <SIM>  
A:Cross-references: UNIPROT:Q9PC23; GB:AE003988; GB:AE003849; NID:99106653; PIDN:AAF8442  
A:Experimental source: strain 9a5c  
R:Simmons, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1611  
C:Superfamily: Escherichia coli hypothetical 48k protein (glnA-fdhE region)

Query Match 2.5%; Score 7; DB 2; Length 401;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 DAEYGLY 240  
Db 157 DAEYGLY 163

## RESULT 17

G90210  
Hypothetical protein purF-2 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: G90210  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awavez, M.J.; Chan-yong, J.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: G90210  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-404 <KUR>  
A:Cross-references: UNIPROT:Q9UX27; GB:AE006641; NID:gl3813800; PIDN:AAK40942.1; GSPDB:CG  
C:Genetics:  
A:Gene: purF-2

Query Match 2.5%; Score 7; DB 2; Length 404;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YKSGIA 55  
Db 35 YKSGIA 41

## RESULT 18

S53916  
SUN4 protein precursor - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein N2411; protein YNL066w; protein YNL1612  
C:Species: Saccharomyces cerevisiae  
C:Date: 08-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C:Accession: S53916; S58712; S62994; S62998; S63945  
R:Poehlmann, R.; Philippsen, P.  
submitted to the EMBL Data Library, April 1995  
A:Reference number: S53896  
A:Accession: S53916  
A:Molecule type: DNA  
A:Residues: 1-420 <POE>  
A:Cross-references: UNIPROT:P53616; EMBL:X86470; NID:g791101; PID:g791122  
R:Bergez, P.; Dolignon, F.; Crouzet, M.  
Yeast 11, 967-974, 1995  
A:Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV  
A:Reference number: S58711, MUID:96021608; PMID:8533472  
A:Accession: S58712  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-420 <BER>  
A:Cross-references: EMBL:U12141; NID:gl314216; PIDN:AAA99645.1; PID:g9994821  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
R:Bergez, P.; Dolignon, F.; Crouzet, M.  
submitted to the Protein Sequence Database, April 1996  
A:Reference number: S62975  
A:Accession: S62994  
A:Molecule type: DNA  
A:Residues: 1-420 <BEF>  
A:Cross-references: EMBL:Z71342; NID:gl301944; PID:gl301945; MIPS:YNL066w  
A:Experimental source: strain S288C  
R:Poehlmann, R.; Philippsen, P.  
submitted to the Protein Sequence Database, April 1996  
A:Reference number: S62997  
A:Accession: S62998  
A:Molecule type: DNA  
A:Residues: 1-420 <POW>

A/Cross-references: EMBL:Z71342; NID:g1301944; PID:g1301945; MIPS:YNL066w  
 A/Experimental source: strain S288C  
 R;Poehlmann, R.; Philippsen, P.  
 Yeast 12, 391-402, 1996  
 A/Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals 12  
 A/Reference number: S63925; MUID:96267764; PMID:8701611  
 A/Accession: S63945  
 A/Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-420 <POF>  
 A/Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60196.1; PID:g791122  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995  
 C/Genetics:  
 A/Gene: SGD:SUN4  
 A/Cross-references: SGD:S0005010; MIPS:YNL066w  
 A/Map position: 14L  
 A/Genome: nuclear  
 C/Superfamily: Saccharomyces NCA3 protein  
 C/Keywords: mitochondrion  
 F:1-46/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
 F:46-420/Product: SUN4 protein #status predicted <MAT>

Query Match 2.5%; Score 7; DB 2; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 VAVTVYV 37  
 |||||  
 Db 47 VAVTVYV 53

RESULT 19  
 H84806  
 hypothetical protein At2g38590 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C/Accession: H84806  
 M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 408, 761-768, 1999  
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A/Reference number: H84420; MUID:20083487; PMID:10617197  
 A/Accession: H84806  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-424 <STO>  
 A/Cross-references: UNIPROT:Q9ZV11; GB:AE002093; NID:g3786013; PIDN:AAC67359.1; GSPDB:GN  
 C/Genetics:  
 A/Gene: At2g38590  
 A/Map position: 2  
 C/Superfamily: Arabidopsis thaliana hypothetical protein T1F15.9

Query Match 2.5%; Score 7; DB 2; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CFLKEDD 62  
 |||||  
 Db 122 CFLKEDD 128

RESULT 20  
 G71272  
 iron-sulfur cofactor synthesis protein nifS2 TP0863 [similarity] - syphilis spirochete  
 N/Contains: L-cysteine sulfurtransferase (EC 2.8.1.-)  
 C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C/Accession: G71272  
 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD  
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
 . Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
 A/Reference number: A71250; MUID:98332770; PMID:9665876  
 A/Accession: G71272  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-427 <COL>  
 A/Cross-references: UNIPROT:O83835; GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AAC6582  
 A/Experimental source: strain Nichols  
 C/Genetics:  
 A/Gene: TP0863  
 C/Superfamily: nitrogen fixation protein nifs  
 C/Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase  
 F:232/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted  
 F:374/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 2.5%; Score 7; DB 2; Length 427;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGTGRGS 133  
 |||||  
 Db 166 TGTGRGS 172

RESULT 21  
 E84192  
 zinc metalloproteinase homolog [imported] - Halobacterium sp. NRC-1  
 C/Species: Halobacterium sp. NRC-1  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C/Accession: E84192  
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.  
 ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor  
 Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
 A/Title: Genome sequence of Halobacterium species NRC-1.  
 A/Reference number: E84160; MUID:20504483; PMID:11016950  
 A/Accession: E84192  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-428 <STO>  
 A/Cross-references: UNIPROT:Q9HSA2; GB:AE004437; NID:g10579955; PIDN:AGI8905.1; GSPDB:G  
 C/Genetics:  
 A/Gene: caax

Query Match 2.5%; Score 7; DB 2; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 SSRSQHS 162  
 |||||  
 Db 237 SSRSQHS 243

RESULT 22  
 B72109  
 GMP synthase CP0599 [imported] - Chlamydomophila pneumoniae (strains CWL029 and AR39)  
 C/Species: Chlamydomophila pneumoniae; Chlamydia pneumoniae  
 C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C/Accession: B72109; E81558  
 R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
 Nature Genet. 21, 385-389, 1999  
 A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
 A/Reference number: A72000; MUID:99206606; PMID:10192388  
 A/Accession: B72109  
 A/Molecule type: DNA  
 A/Residues: 1-429 <ARN>  
 A/Cross-references: UNIPROT:Q9Z913; GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD1832  
 A/Experimental source: strain CWL029  
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.  
 ; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
 Nucleic Acids Res. 28, 1397-1406, 2000  
 A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: E81558

A:Molecule type: DNA

A:Residues: 1-429 <REA>

A:Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38415.1; PID:g718951

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: guaA; CP0599

C:Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology

F;11-194/Domain: trpG homology <TRG>

Query Match 2.5%; Score 7; DB 2; Length 429;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161

Db 248 ESSRSRGH 254

RESULT 23

C86512

GMP synthase [imported] - Chlamydomophila pneumoniae (strain J138)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: C86512

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: AB6491; MUID:20330349; PMID:10871362

A:Accession: C86512

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-429 <STO>

A:Cross-references: UNIPROT:Q92913; GB:BA000008; NID:g8978544; PIDN:BAA98381.1; GSPDB:GN

A:Experimental source: strain J138

C:Genetics:

A:Gene: guaA

C:Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology

Query Match 2.5%; Score 7; DB 2; Length 429;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161

Db 248 ESSRSRGH 254

RESULT 24

AF2539

manganese transport protein all7601 [imported] - Nostoc sp. (strain PCC 7120) plasmid pC

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C:Accession: AF2539

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AF2539

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-442 <KUR>

A:Cross-references: UNIPROT:Q92SB0; GB:AF003602; PIDN:BAF77244.1; PID:g17134686; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all7601

A:Genome: plasmid

C:Superfamily: natural resistance-associated macrophage protein 1

Query Match 2.5%; Score 7; DB 2; Length 442;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 LQSLCV 31

Db 76 LQSLCV 82

RESULT 25

T39359

probable udp-n-acetylglucosamine pyrophosphorylase - fission yeast (Schizosaccharomyces

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T39359

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.

submitted to the EMBL Data Library, March 1999

A:Reference number: Z21848

A:Accession: T39359

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-475 <WOO>

A:Cross-references: UNIPROT:O94617; EMBL:AL035675; PIDN:CAB38688.1; GSPDB:GN00067; SPDB:SF

A:Experimental source: strain 972h-; cosmid c1289

C:Genetics:

A:Gene: SPDB:SPBC1289.08

A:Map position: 2

Query Match 2.5%; Score 7; DB 2; Length 475;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETIS 101

Db 168 TSEETIS 174

RESULT 26

T19496

hypothetical protein C27A7.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 26-May-2000

C:Accession: T19496

R;Harris, B.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19132

A:Accession: T19496

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-511 <WIL>

A:Cross-references: EMBL:Z81041; PIDN:CAB02786.1; GSPDB:GN00023; CESP:C27A7.2

A:Experimental source: clone C27A7

C:Genetics:

A:Gene: CESP:C27A7.2

A:Map position: 5

A:Introns: 44/3; 87/2; 130/2; 164/3; 203/2; 273/3; 325/1; 369/2

C:Superfamily: Caenorhabditis elegans hypothetical protein F07G11.3

Query Match 2.5%; Score 7; DB 2; Length 511;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YKSGIA 55

Db 120 YKSGIA 126

RESULT 27

A47503

epoxide hydrolase (EC 3.3.2.3), cytosolic - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A47503; S17104; S19319

R;Knehr, M.; Thomas, H.; Arand, M.; Gebel, T.; Zeller, H.D.; Oesch, F.

```

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22360
R/White, S.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z19553
A:Accession: T22360
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-710 <WIL>
A:Cross-references: UNIPROT:Q9VTS0; EMBL:Z99171; PIDN:CAB16314.1; GSPDB:GN00019; CESP:F4;
A:Experimental source: clone F47G4
C/Genetics:
A:Gene: CESP:F47G4.2
A/Map position: 1
A/Introns: 20/1; 131/3; 220/2; 273/1; 380/2; 577/2

Query Match          2.5%; Score 7; DB 2; Length 710;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 ILRTSEE 98
    |||||
Db 647 ILRTSEE 653

RESULT 30
AE3032
conserved hypothetical protein Atu3866 [imported] - Agrobacterium tumefaciens (strain C58)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AE3032
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan;
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepsan, W.; Perry, M.; Gordon-Kamm, I.;
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE3032
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-801 <KUR>
A:Cross-references: UNIPROT:Q8U963; GB:AE008689; PIDN:AAL44675.1; PID:gl17742302; GSPDB:G1
A:Experimental source: strain C58 (Dupont)
C/Genetics:
A:Gene: Atu3866
A/Map position: linear chromosome

Query Match          2.5%; Score 7; DB 2; Length 801;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
    |||||
Db 216 ASFFGAF 222

RESULT 31
G98253
hypothetical protein AGR_L_1958 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: G98253
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G98253
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-801 <KUR>

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A;Cross-references: UNIPROT:Q8U963; GB:AE007870; PIDN:AAK09553.1; PID:gl3159435; GSPDB:G  
C;Genetics:  
A;Gene: AGK\_L\_1958  
A;Map position: linear chromosome

Query Match 2.5%; Score 7; DB 2; Length 801;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278  
|||||  
Db 216 ASFFGAF 222

RESULT 32  
T20430  
hypothetical protein E03A3.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T20430  
R;Gardner, A.  
submitted to the EMBL Data Library, October 1994  
A;Reference number: Z19274  
A;Accession: T20430  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-809 <WIL>  
A;Cross-references: UNIPROT:Q19046; EMBL:Z38112; PIDN:CAA86232.1; GSPDB:GNO0021; CESP:EQ  
C;Genetics:  
A;Gene: CESP:E03A3.2  
A;Map position: 3  
A;Introns: 49/3; 144/1; 319/2; 376/3; 484/2; 540/3; 573/2; 612/3; 720/3; 776/3

Query Match 2.5%; Score 7; DB 2; Length 809;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 EYGLYSI 242  
|||||  
Db 756 EYGLYSI 762

RESULT 33  
D90183  
ATP-dependent helicase [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: D90183  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrett, R.A.; Ragan, M.A.; SENSEN, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: D90183  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-913 <KUR>  
A;Cross-references: UNIPROT:Q980C0; GB:AE006641; NID:gl3813545; PIDN:AAK40723.1; GSPDB:G  
C;Genetics:  
A;Gene: S800394

Query Match 2.5%; Score 7; DB 2; Length 913;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 ENDRIFV 258  
|||||  
Db 517 ENDRIFV 523

RESULT 34

A;Cross-references: UNIPROT:Q8C12.10 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T15683  
R;Miller, N.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid C28C12.  
A;Reference number: Z18387  
A;Accession: T15683  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-926 <WIL>  
A;Cross-references: UNIPROT:Q18284; EMBL:U40797; NID:gl065916; PID:gl065927; PIDN:AA8375  
A;Experimental source: strain Bristol N2; clone C28C12  
C;Genetics:  
A;Gene: CESP:C28C12.10  
A;Map position: 4  
A;Introns: 18/3; 98/2; 173/2; 206/3; 298/3; 405/3; 488/3; 727/3; 761/1; 828/2

Query Match 2.5%; Score 7; DB 2; Length 926;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 DEESMNS 75  
|||||  
Db 122 DEESMNS 128

RESULT 35  
JH0109  
glycoprotein 14 precursor - equine herpesvirus 1  
C;Species: equine herpesvirus 1  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C;Accession: JH0109  
R;Guo, P.  
Gene 87, 249-255, 1990  
A;Title: Characterization of the gene and an antigenic determinant of equine herpesvirus  
A;Reference number: JH0109; MUID:90236317; PMID:1692002  
A;Accession: JH0109  
A;Molecule type: DNA  
A;Residues: 1-979 <GUO>  
A;Cross-references: UNIPROT:P25218; GB:M34861; NID:g330900; PIDN:AAA46086.1; PID:g330901  
A;Note: Glycoprotein 14 is homologous to corresponding glycoprotein of pseudorabies, bov  
C;Genetics:  
A;Gene: gp14  
C;Superfamily: herpesvirus glycoprotein B  
C;Keywords: glycoprotein; transmembrane protein  
F;1-86/Domain: signal sequence #status predicted <SIG>  
F;87-979/Product: glycoprotein 14 #status predicted <MAT>  
F;831-871/Region: hydrophobic  
F;165,275,380,423,457,514,560,727,749,951,970/Binding site: carbohydrate (Asn) (covalent)

Query Match 2.5%; Score 7; DB 2; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 SGIACFL 58  
|||||  
Db 839 SGIACFL 845

RESULT 36  
E88465  
protein B0244.6 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: E88465  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gac/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A:Accession: E88465  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-982 <STO>  
 A:Cross-references: UNIPROT:Q09965; GB:chr\_III; PIDN:AAA68379.1; PID:9861359; GSPDB:GN000019; CESP:F26H9.8  
 C:Genetics:  
 A:Gene: B0244.6  
 A:Map position: 3

Query Match 2.5%; Score 7; DB 2; Length 982;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNLTSS 138  
 DB 461 RSNLTSS 467  
 |||||

RESULT 37  
 T36031  
 excinuclease ABC chain A SCC54.18c [similarity] - Streptomyces coelicolor  
 N:Contains: excision endonuclease ABC (EC 3.1.1.-) chain A  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: T36031  
 R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, March 1999  
 A:Reference number: Z21581  
 A:Accession: T36031  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1014 <SES>  
 A:Cross-references: UNIPROT:Q92507; EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN000070; SCOE  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: uvrA; SCOE:SCC54.18c  
 C:Superfamily: excinuclease ABC chain A; ATP-binding cassette homology  
 C:Keywords: ATP; DNA binding; DNA repair; hydrolase; nucleotide binding; P-loop  
 F:32-39/Region: nucleotide-binding motif A (P-loop)  
 F:645-652/Region: nucleotide-binding motif A (P-loop)

Query Match 2.5%; Score 7; DB 2; Length 1014;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117  
 DB 153 SPLVRER 159  
 |||||

RESULT 38  
 T19214  
 UDP-glucose-glycoprotein glucosyltransferase (EC 2.4.1.-) precursor F26H9.8 - Caenorhab  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T19214; T21444  
 R:Barlow, K.  
 submitted to the EMBL Data Library, November 1996  
 A:Reference number: Z19091  
 A:Accession: T19214  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1377 <WIL>  
 A:Cross-references: UNIPROT:P01854; EMBL:Z01467; PIDN:CAB03874.1; GSPDB:GN000019; CESP:F2  
 A:Experimental source: clone C12C8  
 R:Baynes, C.  
 submitted to the EMBL Data Library, November 1996

A:Reference number: Z19422  
 A:Accession: T21444  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1377 <W12>

A:Cross-references: EMBL:Z81516; PIDN:CAB04207.1; GSPDB:GN000019; CESP:F26H9.8  
 A:Experimental source: clone F26H9  
 C:Genetics:  
 A:Gene: CESP:F26H9.8  
 A:Map position: 1  
 A:Introns: 40/2; 70/1; 152/2; 318/2; 429/3; 494/2; 538/3; 564/3; 625/3; 654/3; 782/3; 828/3  
 C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase

Query Match 2.5%; Score 7; DB 2; Length 1377;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 NLHLRNG 172  
 DB 1014 NLHLRNG 1020  
 |||||

RESULT 39  
 T3236  
 hypothetical protein T10H9.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T3236  
 R:Greco, T.; Bradshaw, H.; O'Brien, D.  
 submitted to the EMBL Data Library, May 1998  
 A:Description: The sequence of C. elegans cosmid T10H9.  
 A:Reference number: Z21306  
 A:Accession: T3236  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1414 <GR>  
 A:Cross-references: UNIPROT:O76411; EMBL:AF067949; PIDN:AAC19236.1; GSPDB:GN000023; CESP:1  
 A:Experimental source: strain Bristol N2; clone T10H9  
 C:Genetics:  
 A:Gene: CESP:T10H9.2  
 A:Map position: 5

Query Match 2.5%; Score 7; DB 2; Length 1414;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 RGPQVVA 123  
 DB 1110 RGPQVVA 1116  
 |||||

RESULT 40  
 E64477  
 replication factor C homolog - Methanococcus jannaschii  
 C:Species: Methanococcus jannaschii  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C:Accession: E64477  
 R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.  
 Reisch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
 Science 273, 1058-1073, 1996  
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.  
 A:Reference number: A64300; MUID:96337999; PMID:8688087  
 A:Accession: E64477  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1847 <BUL>  
 A:Cross-references: UNIPROT:Q58817; GB:U67583; GB:L77117; NID:92826409; PIDN:AAB99433.1;  
 C:Genetics:  
 A:Map position: REV1393176-1387633  
 A:Start codon: TTG

Query Match 2.5%; Score 7; DB 2; Length 1847;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 IPFLKEN 253

Db 877 IPFLKEN 883

## RESULT 41

T43262

calcium channel alpha-1 chain, L-type - Stylophora pistillata

C:Species: Stylophora pistillata

C&gt;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T43262

R:Zoccola, D.; Tambutte, E.; Senegas-Balazs, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J.

Gene 227, 157-167, 1999

A:Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, Stylo

A:Reference number: 222375; MUID:99148007; PMID:10023047

A:Accession: T43262

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1891 &lt;ZOC&gt;

A:Cross-references: UNIPROT:O97017; EMBL:U64465; NID:G4204977; PID:G4204978; PIDN:AAH114

C:Genetics:

A:Gene: CACHL

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 1891;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 FLKEDDS 63

Db 1621 FLKEDDS 1627

## RESULT 42

B81192

hemagglutinin/hemolysin-related protein NMB0497 [imported] - Neisseria meningitidis (str

C:Species: Neisseria meningitidis

C&gt;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: B81192

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: B81192

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1975 &lt;TET&gt;

A:Cross-references: UNIPROT:Q9K0S7; GB:AF002406; GB:AE002098; NID:G7225720; PIDN:AAF4092

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0497

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 1975;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129

Db 557 AAHITGT 563

## RESULT 43

G81044

hemagglutinin/hemolysin-related protein NMB1779 [imported] - Neisseria meningitidis (str

C:Species: Neisseria meningitidis

C&gt;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: G81044

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: G81044

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1995 &lt;TET&gt;

A:Cross-references: UNIPROT:Q9JY23; GB:AE002527; GB:AE002098; NID:G7227023; PIDN:AAF42111

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1779

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 1995;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129

Db 560 AAHITGT 566

## RESULT 44

B81989

hypothetical protein NMA0698 [imported] - Neisseria meningitidis (strain Z2491 serogroup

C:Species: Neisseria meningitidis

C&gt;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004

C:Accession: B81989

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: B81989

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2015 &lt;PAR&gt;

A:Cross-references: UNIPROT:Q9JRD2; GB:AL162753; GB:AL157959; NID:G7379120; PIDN:CA883974

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA0688

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 2015;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129

Db 560 AAHITGT 566

## RESULT 45

GNWVW

genome polyprotein - Murray Valley encephalitis virus (strain Australia)

N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS1

a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: Murray Valley encephalitis virus

C&gt;Date: 30-Jun-1988 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004

C:Accession: A24635; A60288

R:Dalgarno, L.; Trent, D.W.; Strauss, J.H.; Rice, C.M.

J. Mol. Biol. 187, 309-323, 1986

A:Title: Partial nucleotide sequence of the Murray Valley encephalitis virus genome: com

A:Reference number: A24635; MUID:86200215; PMID:3009829

A:Accession: A24635

A:Molecule type: genomic RNA

A:Residues: 1-1780 &lt;DAL&gt;

A:Cross-references: UNIPROT:P05769; GB:X03467; NID:G59329; PIDN:CAA27184.1; PID:G755731

R:Lee, E.; Fernon, C.; Simpson, R.; Weir, R.C.; Rice, C.M.; Dalgarno, L.

Virus Genes 4, 197-213, 1990

A:Title: Sequence of the 3' half of the Murray Valley encephalitis virus genome and map

A:Reference number: A60288; MUID:91102934; PMID:1702914

A:Accession: A60288

A:Molecule type: genomic RNA



A:Residues: 1504-1778,'V',1780-3434 <LEE>  
 C:Superfamily: yellow fever virus genome polyprotein  
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;  
 F:1-125/Product: capsid protein #status predicted <CAP>  
 F:126-292/Product: membrane protein precursor #status predicted <GLC>  
 F:126-217/Domain: nonterminal signal sequence #status predicted <SIG>  
 F:218-292/Product: membrane protein #status predicted <GLM>  
 F:278-292/Domain: transmembrane #status predicted <TN1>  
 F:293-793/Product: envelope protein #status predicted <ENV>  
 F:773-791/Domain: transmembrane #status predicted <TN2>  
 F:794-1205/Product: nonstructural protein NS1 #status predicted <NS1>  
 F:1206-1372/Product: nonstructural protein NS2a #status predicted <NS2>  
 F:1373-1503/Product: nonstructural protein NS2b #status predicted <NS2>  
 F:1504-2122/Product: nonstructural protein NS3 #status predicted <NS3>  
 F:1697-1704/Region: nucleotide-binding motif A (P-loop)  
 F:1784-1789/Region: nucleotide-binding motif B  
 F:1788-1791/Region: DEAH motif  
 F:2123-2414/Product: nonstructural protein NS4a #status predicted <NS4>  
 F:2415-2529/Product: nonstructural protein NS4b #status predicted <NS4>  
 F:2530-3434/Product: nonstructural protein NS5 #status predicted <NS5>  
 F:73,140,446/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.5%; Score 7; DB 1; Length 3434;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIFTVLL 26  
 |||||  
 Db 278 VIFTVLL 284

RESULT 46  
 T04365  
 ethylene responsive element binding protein - rice  
 C:Species: Oryza sativa (rice)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T04365  
 R:Kim, C.Y.; Jeong, S.Y.; Choe, M.S.; Cheong, Y.H.; Han, C.D.; Cho, M.J.  
 submitted to the EMBL Data Library, March 1997  
 A:Description: Isolation and characterization of early inducible rice genes by a fungal  
 A:Reference number: Z15314  
 A:Accession: T04365  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-47 <KIM>  
 A:Cross-references: UNIPROT:O24522; EMBL:U95216; NID:g2443456; PIDN:AAB71382.1; PID:g244

A:Gene: EREBP1

Query Match 2.1%; Score 6; DB 2; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 86;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSL 29  
 |||||  
 Db 2 VLLQSL 7

RESULT 47  
 S78202  
 H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - fission yeast (Schizosacchar

C:Species: mitochondrion Schizosaccharomyces pombe  
 C:Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 03-Jun-2002  
 C:Accession: S78202  
 R:Lang, B.F.  
 submitted to the EMBL Data Library, August 1990  
 A:Description: The mitochondrial genome of the fission yeast Schizosaccharomyces pombe:  
 chizosaccharomyces pombe and Aspergillus nidulans.  
 A:Reference number: S78195  
 A:Accession: S78202  
 A:Molecule type: DNA  
 A:Residues: 1-48 <LAN>  
 A:Cross-references: EMBL:X54421; NID:g13639; PID:g1334456

A:Experimental source: strain ad7-50h  
 C:Genetics:  
 A:Gene: atp8  
 A:Genome: mitochondrion  
 A:Genetic code: SGC2  
 C:Superfamily: yeast H+-transporting ATP synthase protein 8  
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxid

Query Match 2.1%; Score 6; DB 2; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 IFTVLL 26  
 |||||  
 Db 19 IFTVLL 24

RESULT 48  
 AF2105  
 hypothetical protein asl2397 [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AF2105  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AF2105  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-55 <KUR>  
 A:Cross-references: UNIPROT:O8YUF3; GB:BA000019; PIDN:BA074096.1; PID:g17131489; GSPDB:G

A:Experimental source: strain PCC 7120

Query Match 2.1%; Score 6; DB 2; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 FLSNLH 168  
 |||||  
 Db 35 FLSNLH 40

RESULT 49  
 C60157  
 hypothetical protein 2 (prtM 5' region) - Lactococcus lactis subsp. cremoris plasmid pMW1  
 C:Species: Lactococcus lactis subsp. cremoris  
 C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
 C:Accession: C60157  
 R:Haandrikman, A.J.; van Leeuwen, C.; Kok, J.; Vos, P.; de Vos, W.M.; Venema, G.  
 Appl. Environ. Microbiol. 56, 1890-1896, 1990  
 A:Title: Insertion elements on lactococcal proteinase plasmids.  
 A:Reference number: A60157; MUID:90343335; PMID:2166472  
 A:Accession: C60157  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-56 <HAA>  
 A:Cross-references: UNIPROT:Q48694; GB:M37396; NID:g149472; PIDN:AAA25212.1; PID:g149474

A:Genome: plasmid pMW05

Query Match 2.1%; Score 6; DB 2; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSL 29  
 |||||  
 Db 39 VLLQSL 44



```

RESULT 50
C97621
hypothetical protein AGR_C_3957 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: C97621
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: C97621
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-62 <KUR>
A/Cross-references: UNIPROT:Q8U558; GB:AB007869; PIDN:AAK87924.1; PID:g15157324; GSPDB:G
C/Genetics:
A/Gene: AGR_C_3957
A/Map position: circular chromosome

Query Match      2.1%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      118 GQORVA 123
          |||||
Db       7 GQORVA 12

RESULT 51
AG0025
probable bacterioferritin-associated ferredoxin bfd [imported] - Yersinia pestis (strain
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AG0025
R/Parthill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AG0025
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-64 <KUR>
A/Cross-references: UNIPROT:Q8ZJB1; GB:AL590842; PIDN:CAC89066.1; PID:g15978306; GSPDB:G
C/Genetics:
A/Gene: bfd
C/Superfamily: yheA protein

Query Match      2.1%; Score 6; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 QLRQLV 88
          |||||
Db      28 QLRQLV 33

RESULT 52
AC00774
hypothetical protein STY2363 [imported] - Salmonella enterica subsp. enterica serovar Ty
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AC00774
R/Farkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

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```

A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AC0774
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-65 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD02513.1; PID:g16503375; GSPDB:GN00176
C/Genetics:
A/Gene: STY2363

```

```

Query Match      2.1%; Score 6; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      196 IKENTK 201
          |||||
Db       46 IKENTK 51

```

# RESULT 53

```

C91249
hypothetical protein ECs4963 [imported] - Escherichia coli (strain O157:H7, substrain RI:
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: C91249
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
Gagawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: C91249
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-85 <HAY>
A/Cross-references: UNIPROT:Q8X322; GB:BA000007; PIDN:BA838386.1; PID:g13364439; GSPDB:G
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECs4963

```

```

Query Match      2.1%; Score 6; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      105 EKOONI 110
          |||||
Db       31 EKOONI 36

```

# RESULT 54

```

S78744
protein YDR363w-a - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 09-Jul-2004
C/Accession: S78744
R/Du, Z.

```

Submitted to the EMBL Data Library, June 1995

```

A/Description: The sequence of S. cerevisiae cosmid 9476.
A/Reference number: S61148
A/Accession: S78744
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-89 <DUZ>
A/Cross-references: UNIPROT:O94742; EMBL:U28372; MIPS:YDR363w-a
C/Genetics:
A/Gene: SGD:HOD1
A/Cross-references: SGD:S0007235
A/Map position: 4R

```

```

Query Match      2.1%; Score 6; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      38 FTNELK 43
          |||||

```

Db 73 FTNELK 78

RESULT 55

B82311 conserved hypothetical protein VC0527 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C:Species: *Vibrio cholerae*

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C:Accession: B82311

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, P.L.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; PMID:20406833; PMID:10952301

A:Accession: B82311

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-96 <HEI>

A:Cross-references: UNIPROT:Q9KUD3; GB:AE004139; GB:AE003852; NID:g9654953; PIDN:AAF9369

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0527

A:Map position: 1

C:Superfamily: hypothetical protein H10673

Query Match 2.1%; Score 6; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 NLHRLN 171

|||||

Db 47 NLHRLN 52

RESULT 56

AE3205 transposase tnp [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont) plasmid AT

C:Species: *Agrobacterium tumefaciens*

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C:Accession: AE3205

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, K.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.; E.W.

A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A:Reference number: AB2577; PMID:21608550; PMID:11743193

A:Accession: AE3205

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-96 <KUR>

A:Cross-references: UNIPROT:Q8UUV4; GB:AE008687; PIDN:AAU46059.1; PID:g17743819; GSPDB:G

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: tnp

A:Genome: plasmid

Query Match 2.1%; Score 6; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 LVRERG 118

|||||

Db 17 LVRERG 22

RESULT 57

G91248 hypothetical protein ECs4959 [imported] - *Escherichia coli* (strain O157:H7, substrain R)

C:Species: *Escherichia coli*

C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C:Accession: G91248

R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genome organization

A:Reference number: A99629; PMID:21156231; PMID:11258796

A:Accession: G91248

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <HAY>

A:Cross-references: UNIPROT:Q8X328; GB:BA000007; PIDN:BAE38382.1; PID:g13364435; GSPDB:G

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs4959

Query Match 2.1%; Score 6; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 SFFGAF 278

|||||

Db 15 SFFGAF 20

RESULT 58

C95337 probable cytochrome C fragment [imported] - *Sinorhizobium meliloti* (strain 1021) magapla

C:Species: *Sinorhizobium meliloti*

C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C:Accession: C95337

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*

A:Reference number: A95262; PMID:21396509; PMID:11481432

A:Accession: C95337

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <KUR>

A:Cross-references: UNIPROT:Q92Z89; GB:AE006469; PIDN:AAK65261.1; PID:g14523712; GSPDB:G

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, heault, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A:Reference number: A96039; PMID:21368234; PMID:11474104

C:Genetics:

A:Gene: SWall13

A:Genome: plasmid

Query Match 2.1%; Score 6; DB 2; Length 102;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 VAAHIT 127

|||||

Db 96 VAAHIT 101

RESULT 59

E69832 conserved hypothetical protein yhgB - *Bacillus subtilis*

N; Alternate names: hypothetical protein Y (pbpf 5' region)

C:Species: *Bacillus subtilis*

C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C:Accession: E69832; C40614

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi

C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Brrington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen-  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
V, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: E59832  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-104 <KUN>  
A;Cross-references: UNIPROT:P38048; GB:Z99109; GB:AL009136; NID:G2633260; PIDN:CAB12849.  
A;Experimental source: strain 168  
R;Popham, D.L.; Setlow, P.  
J. Bacteriol. 175, 4870-4876, 1993  
A;Title: Cloning, nucleotide sequence, and regulation of the *Bacillus subtilis* pbpF gene  
A;Reference number: A40614; MUID:93328693; PMID:8335642  
A;Accession: C40614  
A;Molecule type: DNA  
A;Residues: 1-67 <POP>  
A;Cross-references: GB:U0630  
C;Genetics:  
A;Gene: yhgB

Query Match 2.1%; Score 6; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 LMKSR 227

Db 25 LMKSR 30

RESULT 60

B86818  
hypothetical protein ypiJ [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)  
C;Species: *Lactococcus lactis* subsp. *lactis*  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: B86818  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s  
A;Reference number: A86825; MUID:21235186; PMID:11337471  
A;Accession: B86818  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-105 <STO>  
A;Cross-references: UNIPROT:Q9CFD5; GB:AE005176; PID:gl2724547; PIDN:AAK05644.1; GSPDB:G  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: ypiJ

Query Match 2.1%; Score 6; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 SSPNSK 142

Db 42 SSPNSK 47

RESULT 61

S09964  
IG kappa chain V-J region (105-2H) - mouse (fragment)  
C;Species: *Mus musculus* (house mouse)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000  
C;Accession: S09964

R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
Eur. J. Immunol. 20, 771-777, 1990  
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies  
A;Reference number: S09955; MUID:90269328; PMID:2347362  
A;Accession: S09964  
A;Molecule type: mRNA  
A;Residues: 1-107 <REI>

A;Cross-references: EMBL:X51852; NID:G55393; PIDN:CAA36145.1; PID:93030229  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMW>

Query Match 2.1%; Score 6; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 TISTVQ 104

Db 74 TISTVQ 79

RESULT 62

A44887  
glucose transporter isoform 1, GLUT 1 - mouse (fragment)  
C;Species: *Mus musculus* (house mouse)  
C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 24-Sep-1999  
C;Accession: A44887  
R;Hogan, A.; Heyner, S.; Charron, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; The  
Development 113, 363-372, 1991  
A;Title: Glucose transporter gene expression in early mouse embryos.  
A;Reference number: A44887; MUID:92111400; PMID:1765007  
A;Accession: A44887  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-107 <HOG>

A;Cross-references: GB:S77924; NID:G242127; PIDN:AAB20846.1; PID:G242128  
A;Experimental source: embryo  
A;Note: this sequence is inconsistent with the nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBIN:77924, NCBI:P:77925)  
C;Superfamily: glucose transport protein

Query Match 2.1%; Score 6; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 IFTVLL 26

Db 80 IFTVLL 85

RESULT 63

F84012  
hypothetical protein BH2902 [imported] - *Bacillus halodurans* (strain C-125)  
C;Species: *Bacillus halodurans*  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: F84012  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: F84012  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-109 <STO>  
A;Cross-references: UNIPROT:Q9K8V0; GB:AP001517; GB:BA000004; NID:gl0175500; PIDN:BA0066  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: BH2902

Query Match 2.1%; Score 6; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 RINGELV 175  
 Db 38 RINGELV 43

RESULT 64  
 AC2887  
 conserved hypothetical protein Atu2536 [imported] - Agrobacterium tumefaciens (strain C58)  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
 C:Accession: AC2887  
 C:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.; E.W.  
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; MUID:21608550; PMID:11743193  
 A:Accession: AC2887  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-112 <KUR>  
 A:Cross-references: UNIPROT:Q8UCG1; GB:AE008688; PIDN:AAL43513.1; PID:gl17741022; GSPDB:G  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: Atu2526  
 A:Map position: circular chromosome

Query Match 2.1%; Score 6; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 HLRNGE 173  
 Db 35 HLRNGE 40

RESULT 65  
 H97662  
 hypothetical protein AGR\_C\_4590 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: H97662  
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A:Reference number: A97359; MUID:21608551; PMID:11743194  
 A:Accession: H97662  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-112 <KUR>  
 A:Cross-references: UNIPROT:Q8UCG1; GB:AE007869; PIDN:AAK8257.1; PID:gl15157717; GSPDB:G  
 C:Genetics:  
 A:Gene: AGR\_C\_4590  
 A:Map position: circular chromosome

Query Match 2.1%; Score 6; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 HLRNGE 173  
 Db 35 HLRNGE 40

RESULT 66  
 B25924  
 Ig kappa chain precursor V region (Ser-b) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 21-Jan-2000  
 C:Accession: B25924

R:Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986  
 A:Title: Structural differences in a single gene encoding the V-kappa-Ser group of light  
 A:Reference number: A94141; MUID:87067464; PMID:3097643  
 A:Accession: B25924  
 A:Molecule type: DNA  
 A:Residues: 1-115 <BOY>  
 A:Cross-references: GB:M14360; NID:gl197464; PIDN:AAA39034.1; PID:gl197465  
 A:Experimental source: strain BALB/C  
 C:Genetics: 17/1  
 A:Introns: 17/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-115/Product: Ig kappa chain V region Ser-b #status predicted <MAT>  
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.1%; Score 6; DB 2; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 TISTVQ 104  
 Db 94 TISTVQ 99

RESULT 67  
 C83166  
 probable chaperone PA3842 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 C:Accession: C83166  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoge  
 A:Reference number: AB2950; MUID:20437337; PMID:10984043  
 A:Accession: C83166  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-116 <STO>  
 A:Cross-references: UNIPROT:Q51450; GB:AE004801; GB:AE004091; NID:g9950011; PIDN:AAG0722;  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA3842  
 C:Superfamily: Yersinia pestis plasmid pCD1 hypothetical protein syce

Query Match 2.1%; Score 6; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 PNDEES 72  
 Db 21 PNDEES 26

RESULT 68  
 F97174  
 hypothetical protein CAC2228 [imported] - Clostridium acetobutylicum  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: F97174  
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
 .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: F97174  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-117 <KUR>  
 A:Cross-references: UNIPROT:Q97GY7; GB:AE001437; PIDN:AAK80185.1; PID:gl5025227; GSPDB:G

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC2228

Query Match 2.1% Score 6; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 NGELVI 176

Db 91 NGELVI 96

RESULT 69

lambda 208 protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus

C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OPMNPV

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004

C;Accession: JQ2032

R;Russell, R.L.Q.; Rohrmann, G.F.

J. Gen. Virol. 74, 1191-1195, 1993

A;Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus lambda 208 protein

A;Reference number: PQ0633; MUID:93286576; PMID:8389803

A;Accession: JQ2032

A;Molecule type: DNA

A;Residues: 1-119 <RUS>

A;Cross-references: UNIPROT:Q05122; DDBJ:D13375; NID:G222217; PIDN:BA02641.1; PID:G222217

C;Superfamily: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus lambda 208 protein

Query Match 2.1% Score 6; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLRQLV 88

Db 90 QLRQLV 95

RESULT 70

D89803 conserved hypothetical protein SA0358 [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C;Accession: D89803

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: D89803

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-122 <KUR>

A;Cross-references: UNIPROT:Q99WK6; GB:BA000018; PID:g13700285; PIDN:BA041583.1; GSPDB:G13700285

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA0358

Query Match 2.1% Score 6; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KEDDSY 64

Db 42 KEDDSY 47

RESULT 71

AH0043

probable lipoprotein YPO0352 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AH0043

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, P.; Dougan, G.; et al, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0043

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-128 <KUR>

A;Cross-references: UNIPROT:Q8ZIV2; GB:AL590842; PIDN:CAC89211.1; PID:gl5978450; GSPDB:G89211.1

C;Genetics:

A;Gene: YPO0352

C;Superfamily: Escherichia coli hypothetical protein o128

Query Match 2.1% Score 6; DB 2; Length 138;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSS 138

Db 35 SNTLSS 40

RESULT 72

D64559

hypothetical protein HP0316 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004

C;Accession: D64559

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N.

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: D64559

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-130 <TOM>

A;Cross-references: UNIPROT:Q25085; GB:AE000549; GB:AE000511; NID:g2313403; PIDN:AA00738;

Query Match 2.1% Score 6; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 FTNELK 43

Db 111 FTNELK 116

RESULT 73

F86829

ribose ABC transporter permease protein rbaD [imported] - Lactococcus lactis subsp. lactis

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004

C;Accession: F86829

R;Solotkin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, S.

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: F86829

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <STO>

A;Cross-references: UNIPROT:Q9CF43; GB:AB005176; PID:g12724648; PIDN:AAK05736.1; GSPDB:G12724648

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: rbaD

C;Superfamily: fucose operon U protein

Job time : 46 secs

Query Match 2.1%; Score 6; DB 2; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 EBIKEN 199  
Db 71 EBIKEN 76

## RESULT 74

F70650  
hypothetical protein RV3069 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: F70650  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Scares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: F70650  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-132 <COL>  
A:Cross-references: UNIPROT:P95089; GB:Z83866; GB:AL123456; NID:g3261691; PIDN:CAB06254.  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV3069  
C:Superfamily: hypothetical protein MJ1523

Query Match 2.1%; Score 6; DB 2; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 GAFLVG 281  
Db 48 GAFLVG 53

## RESULT 75

AC0855  
probable regulatory protein STY3045 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AC0855  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; S.; Mouton, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AC0855  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-134 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAB06026.1; PID:gl6503993; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY3045

Query Match 2.1%; Score 6; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QLVRKM 91  
Db 127 QLVRKM 132

Search completed: June 22, 2005, 06:52:39

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:07:26 ; Search time 175 Seconds  
(without alignments)  
822.253 Million cell updates/sec

Title: US-10-662-429-2  
Perfect score: 281  
Sequence: 1 MAMVEVQGSPSLGQTCVLIV.....NEHLIDMDHEASFFGAFIVG 281

Scoring table:  
OLIGO  
Gapop-60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	281	100.0	281 1	TN10 HUMAN
2	52	18.5	63 2	Q6JSD9
3	29	10.3	287 2	Q8K3G0
4	14	5.0	291 1	TN10 MOUSE
5	13	4.6	304 2	Q7TIF2
6	10	3.6	299 2	Q6DHG9
7	8	2.8	155 2	Q64UG5
8	8	2.8	455 2	Q9HKC2
9	8	2.8	473 2	Q8FUC2
10	8	2.8	474 2	Q6LQD8
11	8	2.8	475 2	Q8S6N3
12	8	2.8	643 2	Q9R293
13	8	2.8	939 2	Q9NG57
14	8	2.8	950 2	O15788
15	8	2.8	1248 2	Q8IBZ8
16	7	2.5	39 2	Q95NV2
17	7	2.5	51 1	INS ORNAN
18	7	2.5	73 2	Q7URQ9
19	7	2.5	88 2	Q8KH11
20	7	2.5	92 2	Q87OH0
21	7	2.5	93 2	Q9HSN3
22	7	2.5	94 2	Q8PMD7
23	7	2.5	96 1	AH4 TOXGO
24	7	2.5	106 2	Q9LW97
25	7	2.5	107 2	Q9Y777
26	7	2.5	112 2	Q932M3
27	7	2.5	121 2	Q7U9A5
28	7	2.5	123 2	Q6V7H3
29	7	2.5	125 2	P72087
30	7	2.5	134 2	Q8MM82
31	7	2.5	155 2	Q9YBC2
				Q9YBC2 aeropyrum p

#### ALIGNMENTS

32	7	2.5	157	2	Q83TUL	staphylococ
33	7	2.5	157	2	Q6GBC3	staphylococ
34	7	2.5	157	2	Q6GITS	staphylococ
35	7	2.5	172	2	Q9N8D4	trypanosoma
36	7	2.5	191	2	Q7R3Y3	giardia lam
37	7	2.5	193	1	YQ05_XANCP	xanthomonas
38	7	2.5	193	1	YR66_XANAC	xanthomonas
39	7	2.5	204	1	LIPB_NITEU	nitrosomonas
40	7	2.5	209	1	GEMI_HUMAN	homo sapien
41	7	2.5	217	2	Q9LTD0	arabidopsis
42	7	2.5	220	2	Q6S8A0	acidovorax
43	7	2.5	220	2	Q89V44	bradyrhizob
44	7	2.5	222	2	Q7MMP6	vibrio vuln
45	7	2.5	222	2	Q8DFN8	vibrio vuln
46	7	2.5	230	2	Q72XY8	bacillus ce
47	7	2.5	231	2	P90611	toxoplasma
48	7	2.5	232	2	Q7PY53	anopheles g
49	7	2.5	232	2	Q6S8B3	acidovorax
50	7	2.5	240	1	CD7_HUMAN	homo sapien
51	7	2.5	240	2	Q64MD3	bacteroides
52	7	2.5	247	2	Q9EZK4	staphylococ
53	7	2.5	247	2	Q99RD5	staphylococ
54	7	2.5	247	2	Q7A004	staphylococ
55	7	2.5	247	2	Q7A3K0	staphylococ
56	7	2.5	247	2	Q6G6H6	staphylococ
57	7	2.5	251	2	Q94262	schizosacch
58	7	2.5	253	2	Q98D64	rhizobium l
59	7	2.5	271	2	Q636T1	bacillus ce
60	7	2.5	271	2	Q81WU0	bacillus an
61	7	2.5	271	2	Q6HF64	bacillus th
62	7	2.5	293	2	Q8ROL0	mus musculus
63	7	2.5	296	1	LGT_CHLCV	chlamydomophi
64	7	2.5	298	2	Q8DXW4	stretococcc
65	7	2.5	298	2	Q8E3I3	stretococcc
66	7	2.5	305	2	Q6KZP1	pictrophilus
67	7	2.5	314	2	Q6Z6A7	oryza sativ
68	7	2.5	318	2	Q96QL7	homo sapien
69	7	2.5	322	2	Q9VI33	drosofila
70	7	2.5	327	2	Q9PEN6	xyella fas
71	7	2.5	329	2	Q9ZKY9	helicobacte
72	7	2.5	343	2	Q7VJZ3	helicobacte
73	7	2.5	354	2	Q84846	chlamydia t
74	7	2.5	354	2	Q9PL80	chlamydia m
75	7	2.5	359	2	Q9AVE6	oryza sativ
76	7	2.5	361	2	Q98SU0	xenopus lae
77	7	2.5	362	1	YE1J CAEEL	caenorhabdi
78	7	2.5	367	1	MANA MYTED	mytilus edu
79	7	2.5	367	2	Q6GLF3	xenopus tro
80	7	2.5	374	2	Q6CW74	kluyveromyc
81	7	2.5	374	2	Q7UJW6	synchococcc
82	7	2.5	375	2	Q8TWS8	methanopyru
83	7	2.5	375	2	Q9L5E1	salmonella
84	7	2.5	376	2	Q6F9S2	acinetobact
85	7	2.5	379	2	Q89SM4	bradyrhizob
86	7	2.5	383	2	Q7NSQ0	photorhabdu
87	7	2.5	389	2	Q9LTH1	arabidopsis
88	7	2.5	395	2	Q68SS3	pleurotus d
89	7	2.5	396	2	Q68SS2	pleurotus d
90	7	2.5	401	2	Q87CC1	xyella fas
91	7	2.5	401	2	Q9PCZ3	xyella fas
92	7	2.5	402	2	Q9H766	homo sapien
93	7	2.5	404	2	Q9UX27	sulfolobus
94	7	2.5	405	2	Q6GPT4	xenopus lae
95	7	2.5	406	2	Q8NZ26	stretococcc
96	7	2.5	406	2	Q99XN8	stretococcc
97	7	2.5	406	2	Q8K5J7	stretococcc
98	7	2.5	414	2	Q8S179	oryza sativ
99	7	2.5	417	2	Q8KIR0	pseudomonas
100	7	2.5	417	2	Q8KIU0	pseudomonas

RESULT 1  
 TN10 HUMAN  
 ID TN10 HUMAN STANDARD; PRT; 281 AA.  
 AC P50591;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related  
 DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).  
 GN Name=TNFSF10; Synonyms=APO2L, TRAIL;  
 OS Homo sapiens (Human).  
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;  
 RX Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,  
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,  
 RA Goodwin R.G.;  
 RT Identification and characterization of a new member of the TNF family  
 RT that induces apoptosis.;  
 RL Immunity 3:673-682(1995).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=96278649; PubMed=86631110; DOI=10.1074/jbc.271.22.12687;  
 RX Fitts R.W., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,  
 RA Ashkenazi A.;  
 RT Induction of apoptosis by Apo-2 ligand, a new member of the tumor  
 RT necrosis factor cytokine family.;  
 RL J. Biol. Chem. 271:12687-12690(1996).  
 RN [3]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.;  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.  
 RP MEDLINE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;  
 RX Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,  
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
 RT Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
 RT complex with death receptor 5.;  
 RL Mol. Cell 4:563-571(1999).  
 RN [5]  
 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.  
 RP PubMed=10542098; DOI=10.1038/14935;  
 RX Mongkoleapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Screaton G.R.;  
 RT Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.;  
 RL Nat. Struct. Biol. 6:1048-1053(1999).

[6]  
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.  
 RX MEDLINE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;  
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,  
 RA Sung Y.C., Oh B.-H.;  
 RT 2.8 Å resolution crystal structure of human TRAIL, a cytokine with  
 RT selective antitumor activity.;  
 RL Immunity 11:253-261(1999).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,  
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and  
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity  
 CC may be modulated by binding to the decoy receptors  
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot  
 CC induce apoptosis.  
 CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per  
 CC trimer.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung  
 CC and prostate.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC  
 DR EMBL; U37518; AAC50332.1; -;  
 DR EMBL; U57059; AAB01233.1; -;  
 DR EMBL; BC032722; AAB32722.1; -;  
 DR PDB; 1D0G; X-ray; A/B/D=114-281.  
 DR PDB; 1D2Q; X-ray; A=114-281.  
 DR PDB; 1D4V; X-ray; B=119-281.  
 DR PDB; 1D66; X-ray; A=91-281.  
 DR PDB; 1DU3; X-ray; D/E/F/J/K/L=114-281.  
 DR Genew; HGNC:11925; TNFSF10.  
 DR H-InvDB; HIX0003863; -;  
 DR MIM; 603598; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0005102; F:receptor binding; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; TAS.  
 DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IEP.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR006052; TNF family.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF 1; 1.  
 DR PROSITE; PS50049; TNF 2; 1.  
 DR 3D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;  
 DR Transmembrane; Zinc.  
 KW DOMAIN 1 17 Cytoplasmic (Potential).  
 KW TRANSMEM 18 38 Signal-anchor for type II membrane  
 FT protein (Potential).  
 FT Extracellular (Potential).  
 FT Zinc.  
 FT DOMAIN 39 281  
 FT METAL 230 230  
 FT STRAND 123 127  
 FT STRAND 149 150  
 FT STRAND 163 165  
 FT STRAND 167 170  
 FT TURN 171 172  
 FT STRAND 173 176  
 FT STRAND 180 193  
 FT TURN 198 199  
 FT STRAND 205 213  
 FT STRAND 220 228



```

FT TURN 233 234
FT STRAND 237 250
FT TURN 252 253
FT STRAND 255 260
FT HELIX 263 265
FT STRAND 266 267
FT TURN 270 272
FT STRAND 274 279
SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;

Query Match 100.0%; Score 281; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-287;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEQGSGLGTCVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKGIACFLKE 60
DB 1 MAMVEQGSGLGTCVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKGIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
QY 181 FYIYSQTYPRFOEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSAKNSCWSKDAEYGLY 240
DB 181 FYIYSQTYPRFOEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSAKNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNHLLDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNHLLDMDHEASFFGAFLVG 281

RESULT 2
Q6JSD9 PRELIMINARY; PRT; 63 AA.
AC Q6JSD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine tumor necrosis factor ligand superfamily member 10
DE (Fragment).
GN Name=TNFSF10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Polvi A., Ruosaari S., Vendelin J., West A., Saarikko I.,
RA Reinikainen A., Hollmen J., Laitinen T., Mannila H., Lahesmaa R.,
RA Kere J.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY312579; AAR16184.1; -
FT NON TER 1
SQ SEQUENCE 63 AA; 7638 MW; 8F0C7936DA5AA6E6 CRC64;

Query Match 18.5%; Score 52; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.7e-46;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TNELKQMDKYSKGIACFLKEDDSYWDNDDESNMSPCWQVKWQLRQLVRK 90
DB 1 TNELKQMDKYSKGIACFLKEDDSYWDNDDESNMSPCWQVKWQLRQLVRK 52

RESULT 3
Q8K3G0 PRELIMINARY; PRT; 287 AA.
ID Q8K3G0
AC Q8K3G0;

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA;
RA Mueller A.M., Giegerich G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY115578; AAM49797.1; -
DR HSSP; PS0591; ID2Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; UNKNOWN_1.
DR PROSITE; PS00449; TNF 2; 1.
SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 10.3%; Score 29; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 KQMVQYIYKYTSYPPDPILLMKSAKNSCWS 232
DB 214 KQMVQYIYKYTSYPPDPILLMKSAKNSCWS 242

RESULT 4
TN10_MOUSE STANDARD; PRT; 291 AA.
ID TN10_MOUSE
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein).
GN Name=TNFSF10; Synonyms=Trail;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT Identification and characterization of a new member of the TNF family
RT that induces apoptosis."
RL Immunity 3:673-682(1995).
CC -I- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF10G/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF10B/OPG that cannot
CC induce apoptosis.
CC -I- SUBUNIT: Homotrimer (By similarity).
CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: Widespread.
CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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DR EMBL; U37522; AAC52345.1; -.  
DR HSSP; P50591; 1D2Q.  
DR MGD; MGI:107414; Tnfsf10.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR008983; TNF-like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF 1; 1.  
DR PROSITE; PS0049; TNF 2; 1.  
KW Apoptosis; Cytokine; Signal-anchor; Transmembrane.  
FT DOMAIN 1 17 Cytoplasmic (Potential).  
FT TRANSMEM 18 38 Signal-anchor for type II membrane  
FT DOMAIN 39 291 Extracellular (Potential).  
FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 5.0%; Score 14; DB 1; Length 291;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIKYKTSYPDPPI 220

DB 217 VQYIKYKTSYPDPPI 230

## RESULT 5

QYITF2 Q7TIF2 PRELIMINARY; PRT; 304 AA.  
AC Q7TIF2;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Tumor necrosis factor related apoptosis inducing ligand.  
GN Names=TRAIL;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Sayed A.A., Horiuchi H., Furusawa S., Mateuda H.;  
RT "Molecular Cloning and Characterization of Chicken Tumor Necrosis  
RT Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis  
RT Inducing Ligand (TRAIL).";  
RL J. Vet. Med. Sci. 66:643-650 (2004).  
DR EMBL; AB114678; BAC79267.1; -.  
DR HSSP; P50591; 1D2Q.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR008983; TNF-like.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF 1; 1.  
DR PROSITE; PS0049; TNF 2; 1.  
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 4.6%; Score 13; DB 2; Length 304;  
Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 180 GFYYISQTYFRF 192  
DB 184 GFYYISQTYFRF 196

## RESULT 6

Q6DHG9 Q6DHG9 PRELIMINARY; PRT; 299 AA.  
AC Q6DHG9;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Zgc:92320.  
GN Name=zgc:92320;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Whole;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Bathe F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Whole;  
RA Strausberg R.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC076005; AAH76005.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR006052; TNF family.  
DR InterPro; IPR008983; TNF-like.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF 1; 1.  
DR PROSITE; PS0049; TNF 2; 1.  
SQ SEQUENCE 299 AA; 33526 MW; BA776793D2F11ED5 CRC64;

Query Match 3.6%; Score 10; DB 2; Length 299;

Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 YYISQTYFR 191

DB 187 YYISQTYFR 196

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RESULT 7
Q64UGS PRELIMINARY; PRT; 155 AA.
AC Q64UGS;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE AenC family transcriptional regulator.
GN ORFNames=BF2117;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamagishi A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2004).
DR EMBL; AF006941; BAD4864.1; -.
SQ SEQUENCE 155 AA; 17962 MW; B66A33A8AF0DD863 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFQEEIKE 198
Db 84 RFQEEIKE 91

RESULT 8
Q9HKC2 PRELIMINARY; PRT; 465 AA.
AC Q9HKC2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical membrane protein.
GN OrderedLocusNames=Ta0679;
OS Thermoplasma acidophilum
OC Archaea; Euryarchaeota; Thermoplasma; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513 (2000).
DR EMBL; AL445065; CAC11817.1; -.
DR InterPro; IPR007272; DUF395.
DR Pfam; PF04143; DUF395; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 465 AA; 51450 MW; 7AE47FAFF0C44B5A CRC64;

Query Match 2.8%; Score 8; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 SFFGAFLV 280
Db 402 SFFGAFLV 409

RESULT 9
Q8FUC2 PRELIMINARY; PRT; 473 AA.
ID Q8FUC2
AC Q8FUC2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CE0098;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriidae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579 (2003).
DR EMBL; AF005214; BAC16908.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 473 AA; 52745 MW; 9BBF8D8DAA8E249 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 LVREGRGP 120
Db 366 LVREGRGP 373

RESULT 10
Q6LQD8 PRELIMINARY; PRT; 474 AA.
ID Q6LQD8
AC Q6LQD8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative oxidoreductase.
GN Names=EC3960; OrderedLocusNames=PBPRA2086;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378669; CAG20488.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR002114; HPr_SerP_S.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 474 AA; 51903 MW; FA1D1AE8EBPCE95 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLIVITTV 24

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Db      412 VLVIVFTV 419
|||||
RESULT 11
Q8S6N3 PRELIMINARY; PRT; 475 AA.
ID Q8S6N3
AC Q8S6N3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative kelch-containing protein.
GN ORFNames=OSUNBa0073L01.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Ziemann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092548; AM18732.1; -
DR EMBL; AB017083; AAP53323.1; -
DR Gramene; Q8S6N3; -
DR InterPro; IPR001810; F-box.
DR InterPro; IPR011043; Gal oxid central.
DR Pfam; PF00646; F-box_1; 2.
DR Pfam; PF01344; Kelch_1; 1.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00612; Kelch; 2.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 475 AA; 51606 MW; 84258271A075D2EE CRC64;

Query Match 2.8%; Score 8; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 LSSPNSKN 143
Db 5 LSSPNSKN 12
|||||
RESULT 12
Q9R293 PRELIMINARY; PRT; 643 AA.
ID Q9R293
AC Q9R293
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Drug transport protein, putative.
GN OrderedLocusNames=DRA0061;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;

Query Match 2.8%; Score 8; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
Db 373 SNTLSSPN 380
|||||
RESULT 14
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; Pubmed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001862; AAF12254.1; -
DR FIR; G75599; G75599.
DR TIGR; DRA0061; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015520; F:tetracycline:hydrogen antiporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0015904; P:tetracycline transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004638; Efflux_EmrB.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR001958; TCR TetA.
DR PRINTS; PR01035; TCR_TetA.
DR PRINTS; PR01036; TCR_TetA.
DR TIGRfams; TIGR00711; efflux_EmrB; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 643 AA; 67778 MW; 4168A0998E467A63 CRC64;

Query Match 2.8%; Score 8; DB 2; Length 643;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLVIVFTV 24
Db 231 VLVIVFTV 238
|||||
RESULT 13
Q9NG57 PRELIMINARY; PRT; 939 AA.
ID Q9NG57
AC Q9NG57
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG1 protein.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260819; AAF69519.1; -
DR InterPro; IPR009011; Man6phph_recept.
SQ SEQUENCE 939 AA; 109367 MW; E896972DC096412D CRC64;

Query Match 2.8%; Score 8; DB 2; Length 939;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
Db 373 SNTLSSPN 380
|||||

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015788 PRELIMINARY; PRT; 950 AA.  
 AC 015788; 950 AA.  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CG1.  
 GN Name=cgl;  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RC STRAIN=HB3;  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=98054002; PubMed=9393853; DOI=10.1016/S0092-8674(00)80447-X;  
 RA Su X., Kirkman L.A., Fujitaka H., Wellem T.E.;  
 RT "Complex polymorphisms in an approximately 330 kDa protein are linked  
 RT to chloroquine-resistant P. falciparum in Southeast Asia and Africa";  
 RL Cell 91:593-603(1997).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=HB3;  
 RA Su X.-Z., Kirkman L.A., Wellem T.E.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF030690; AAC47851.1; -  
 DR FIR; T09076; T09076.  
 DR InterPro; IPR009011; Man6php\_recept.  
 SQ SEQUENCE 950 AA; 110601 MW; ED19FEA3B517A378 CRC64;  
 Query Match 2.8%; Score 8; DB 2; Length 950;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 133 SNTLSSPN 140  
 DB 361 SNTLSSPN 368  
 |||||  
 RESULT 15  
 Q8IBZ8 PRELIMINARY; PRT; 1248 AA.  
 AC Q8IBZ8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cg1 protein.  
 GN Name=PF07\_0035;  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,  
 RA Quail M., Barrall B.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL844506; CAD50843.1; -  
 DR InterPro; IPR009011; Man6php\_recept.  
 SQ SEQUENCE 1248 AA; 146629 MW; FDBE0EBF1DF769C2 CRC64;  
 Query Match 2.8%; Score 8; DB 2; Length 1248;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 133 SNTLSSPN 140  
 DB 670 SNTLSSPN 677  
 |||||  
 RESULT 16  
 Q95NV2 PRELIMINARY; PRT; 39 AA.  
 ID Q95NV2  
 AC Q95NV2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE GM03003P (GM01206P).  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Friese B., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Facleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY060851; AAL28399.1; -  
 DR EMBL; AY060825; AAL28373.1; -  
 DR FlyBase; FBgn0047295; BCDNA:GM01206.  
 SQ SEQUENCE 39 AA; 4446 MW; 432F8F340E895DC6 CRC64;  
 Query Match 2.5%; Score 7; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 TVLLQSL 29  
 DB 25 TVLLQSL 31  
 |||||  
 RESULT 17  
 INS ORNAN STANDARD; PRT; 51 AA.  
 ID INS ORNAN  
 AC Q9TQY7; Q9TQY8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Insulin.  
 GN Name=INS;  
 OS Ornithorhynchus anatinus (Duckbill platypus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.  
 OX NCBI\_TaxID=9258;  
 RN [1]  
 RC SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=97021710; PubMed=8868070;  
 RA Nourse A., Treacy G.B., Shaw D.C., Jeffrey P.D.;  
 RT "Platyus insulin: indications from the amino acid sequence of  
 RT significant differences in structure from porcine insulin.";  
 RL Biol. Chem. Hoppe-Seyler 377:147-153(1996).  
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It  
 CC increases cell permeability to monosaccharides, amino acids and  
 CC fatty acids. It accelerates glycolysis, the pentose phosphate  
 CC cycle, and glycogen synthesis in liver.  
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two  
 CC disulfide bonds.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the insulin family.  
 DR PIR; S63591; S63590.  
 DR HSSP; P01308; LMHJ.  
 DR InterPro; IPR004825; Ins/IGF/relax.  
 DR PRINTS; PR00277; INSULINB.  
 DR SMART; SM00078; IIGF; 1.  
 DR PROSITE; PS00262; INSULIN; 1.  
 KW Direct protein sequencing; Glucose metabolism; Hormone;  
 KW Insulin family.  
 FT CHAIN 1 30 Insulin B chain.  
 FT NON CONS 30 31  
 FT CHAIN 31 51 Insulin A chain.  
 FT DISULFID 7 37 Interchain.  
 FT DISULFID 19 50 Interchain.  
 FT DISULFID 36 41

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SQ  SEQUENCE      51 AA;  5854 MW;  0E4D30265D77EAA3  CRC64;

Query Match      2.5%;  Score 7;  DB 1;  Length 51;
Best Local Similarity 100.0%;  Pred. No. 45;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      178  EKGFPYYI 184
      |||||
Db      21  EKGFPYYI 27

RESULT 18
Q7URQ9
ID  Q7URQ9      PRELIMINARY;      PRT;      73 AA.
DT  01-OCT-2003 (TrEMBLrel. 25, Created)
DT  01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Hypothetical protein.
GN  OrderedLocusNames=RB5505;
OS  Rhodopirellula baltica.
OC  Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC  Planctomycetaceae; Pirellula.
OX  NCBI_TaxID=117;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1;
RX  MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA  Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA  Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA  Schlesner H., Anann R., Reinhardt R.;
RT  "Complete genome sequence of the marine planctomycete Pirellula sp.
RT  strain 1.";
RL  Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR  EMBL; BX294142; CAD74279.1; -.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE      73 AA;  8265 MW;  EF2C586B58E7443F  CRC64;

```

```

Query Match          2.5%; Score 7; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      223 MKSARNS 229
      |||||
      1 MKSARNS 7

DB

RESULT 19
Q8KH11
ID Q8KH11 PRELIMINARY; PRT; 88 AA.
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Conserved hypothetical membrane protein.
GN Name=pBt095;
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22335415; PubMed=12324359;
RX DOI=10.1128/AEM.68.10.5082-5095.2002;
RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.;
RT "Complete sequence and organisation of pBtoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 68:5082-5095(2002).
DR EMBL; AL331825; CAD30135.1; -.
KW Hypothetical protein.
SQ SEQUENCE 88 AA; 10480 MW; 545BF0363F679398 CRC64;

Query Match          2.5%; Score 7; DB 2; Length 88;

```

```

Best Local Similarity 100.0%; Pred. NO. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRQLVR 89
    |||||
Db 19 QLRQLVR 25

RESULT 20
Q870H0 PRELIMINARY; PRT; 92 AA.
AC Q870H0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sun4p (Fragment).
GN Name=SUN4;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=s288c;
RA Zhang Z., Dietrich F.S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY245796; AAP04346.1; -.
FT NON TER 92
SQ SEQUENCE 92 AA; 9444 MW; 6AA4C3BE7C157E67 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. NO. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 VAVTVVY 37
    |||||
Db 47 VAVTVVY 53

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RESULT 21	Q9HSN3	PRELIMINARY;	PRT;	93 AA.
ID	Q9HSN3			
AC	Q9HSN3;			
DT	01-MAR-2001	(T=EMBLrel. 16, Created)		
DT	01-MAR-2001	(T=EMBLrel. 16, Last sequence update)		
DT	01-JUN-2003	(T=EMBLrel. 24, Last annotation update)		
DE	Vng0151c.			
GN	OrderedLocusNames=VNG0151.3, VNG0151C;			
OS	Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).			
OC	Archaea; Euryarchaeota; Halobacteria; Halobacteriales;			
OC	Halobacteriaceae; Halobacterium.			
OX	NCBI_TaxID=64091;			
FP	[1]			
RN	SEQUENCE FROM N.A.			
RF	MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;			
RA	Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,			
RA	Shukla H.D., Lasky S.R., Baliga N.S., Thorson V., Shroga J.,			
RA	Swartzell S., Weir D., Hall J., Dahl T.A., Welki R., Goo Y.A.,			
RA	Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,			
RA	Maddocks D.G., Jablonski P.F., Pohlschroder M., Spudis J.L., Jung K.-H.,			
RA	Iensenbarger T.A., Peck R.P., Daniels C.J., Dennis P.P., Omer A.D.,			
RA	Alam M., Freitas T., Hou S., Daniels C.J., Riley M., Hood L., Dassarma S.,			
RA	Eberhardt H., Lowe T.M., Liang P.,			
RT	"Genome sequence of Halobacterium species NRC-1."			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).			
DR	EMBL; AE004981; AAC18770.1; -.			
DR	PIR; F84175; F84175.			
DR	InterPro; IPR011594; Thioredoxin like.			
DR	ProDom; PD003679; Thioredoxin_like; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 93 AA; 9680 MW; AE968B359F340B49 CRC64;			
	Query Match	2.5%;	Score 7;	DB 2; Length 93;

```

Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 FVSVTNE 263
Db 13 FVSVTNE 19
|||||

RESULT 22
Q8PMD7 PRELIMINARY; PRT; 94 AA.
AC Q8PMD7
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC1492.
GN OrderedLocusNames=XAC1492;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Subbal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AB011781; AM36362.1; -.
KW Complete proteome.
SQ SEQUENCE 94 AA; 11253 MW; A54AD81C115F8F2B CRC64;

Query Match 2.5%; Score 7; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 NDRIFVS 259
Db 65 NDRIFVS 71
|||||

RESULT 23
AH4_TOXGO STANDARD; PRT; 96 AA.
AC Q27001;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antigen H4 (Fragment).
GN Names=H4;
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=RH;
RX MEDLINE=91216437; PubMed=2022319; DOI=10.1016/0378-1119(91)90044-C;

Johnson A.M., Illana S.;
"Cloning of Toxoplasma gondii gene fragments encoding diagnostic
antigens.";
Gene 99:127-132(1991).
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DR EMBL; M57302; AAA30139.1; -.
DR FIR; PS0423; PS0423.
KW Antigen.
FT NON TER 1 34 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 34' 34
SQ SEQUENCE 96 AA; 10853 MW; 69C7C2D14890FA53 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FQEEIKE 198
Db 2 FQEEIKE 8
|||||

RESULT 24
Q9LV97 PRELIMINARY; PRT; 106 AA.
ID Q9LV97
AC Q9LV97;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXK3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20181125; PubMed=10718197;
RX Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
DR EMBL; AB019236; BAA97292.1; -.
SQ SEQUENCE 106 AA; 12377 MW; A85ECD52EP507B4C CRC64;

Query Match 2.5%; Score 7; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 IVIFTVL 25
Db 17 IVIFTVL 23
|||||

RESULT 25
Q97Y77 PRELIMINARY; PRT; 107 AA.
ID Q97Y77
AC Q97Y77;
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein SSO1462.
GN OrderedLocusNames=SSO1462;
OS Sulfolobus solfataricus.

```

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OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awevez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moers A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AB006762; AAK41690.1; -.
DR PIR; C90304; C90304.
DR InterPro; IPR007272; DUF395.
DR Pfam; PF04143; DUF395; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 107 AA; 12018 MW; 9471937E9819A936 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 FFGAFLV 280
DB 46 FFGAFLV 52

RESULT 26
Q932M3 PRELIMINARY; PRT; 112 AA.
AC Q932M3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Truncated resolvase.
GN Name=truncated-res; OrderedLocNames=SAVP030;
GS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OG Plasmid VRSAp.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita N., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003367; BAB47538.1; -.
DR HSSP; P03012; 2RSL.
DR GO; GO:000150; F:recombinase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR006118; Recombinase_S.
DR InterPro; IPR006119; resolvase_N.
DR Pfam; PF00239; Resolvase; 1.
DR PROSITE; PS00397; RECOMBINASES_1; 1.
DR PROSITE; PS00398; RECOMBINASES_2; 1.
KW Complete proteome; Plasmid.
SQ SEQUENCE 112 AA; 12884 MW; 1ABB806BBADF522 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 92;
```

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 FTVLLQS 28
DB 106 FTVLLQS 112

RESULT 27
Q7U9A5 PRELIMINARY; PRT; 121 AA.
AC Q7U9A5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical.
GN OrderedLocNames=SYNMW0353;
OS Synecococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synecococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; EX569689; CAE06868.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 121 AA; 13842 MW; CE9C32B4C63811F5 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 QRVAARI 126
DB 76 QRVAARI 82

RESULT 28
Q6V7H3 PRELIMINARY; PRT; 123 AA.
AC Q6V7H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Downregulated in ovarian cancer 1-mysin-like protein (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Laughlin A.M., Ing N.H.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY349169; AAK24841.1; -.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 13650 MW; 94B630F68E02FF3F CRC64;

Query Match 2.5%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DPNDEES 72
DB 12 DPNDEES 18

RESULT 29
P72087 PRELIMINARY; PRT; 125 AA.
ID P72087
```



AC P72087;  
 DT 01-FEB-1997 (TRENBLrel. 02, Created)  
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
 DE Hemolysin A homolog (Fragment).  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Z2491;  
 RX MEDLINE=97008141; PubMed=8955317; DOI=10.1073/pnas.93.20.11109;  
 RA Tinsley C.R., Nasrif X.;  
 RT "Analysis of the genetic differences between Neisseria meningitidis  
 RT and Neisseria gonorrhoeae: two closely related bacteria expressing two  
 RT different pathogenicities.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11109-11114(1996).  
 DR EMBL; U56741; AAC44481.1; -.  
 FT NON\_TER 1 125  
 FT NON\_TER 125 125  
 SQ SEQUENCE 125 AA; 12834 MW; 92D8F57FD9493496 CRC64;  
  
 Query Match 2.5%; Score 7; DB 2; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 123 AAHITGT 129  
 Db 18 AAHITGT 24  
 |||||  
 |||||  
  
 RESULT 30  
 Q8MM82  
 ID Q8MM82 PRELIMINARY; PRT; 134 AA.  
 AC Q8MM82;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
 DE Hypothetical protein T02C12.4.  
 GN ORFNames=T02C12.4;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Gardner A.E.;  
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Lloyd C.R.;  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z35603; CAD36484.1; JOINED.  
 DR EMBL; Z38112; CAD36484.1; -.  
 DR EMBL; Z35603; CAD36496.1; JOINED.  
 DR EMBL; Z38112; CAD36496.1; JOINED.  
 DR WormBase; WBGene00011369; T02C12.4.  
 DR WormPep; T02C12.4; CE30825.  
 KW Hypothetical protein.  
 SQ SEQUENCE 134 AA; 15340 MW; 1DB9A0AD8814E477 CRC64;  
  
 Query Match 2.5%; Score 7; DB 2; Length 134;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 236 EYGLYSI 242  
 Db 81 EYGLYSI 87  
 |||||  
 |||||  
  
 RESULT 31  
 Q9YBC2  
 ID Q9YBC2 PRELIMINARY; PRT; 155 AA.  
 AC Q9YBC2;  
 DT 01-NOV-1999 (TRENBLrel. 12, Created)  
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Hypothetical protein APE1675.  
 GN OrderedLocusNames=APE1675;  
 OS Aeropyrum pernix.  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;  
 OC Desulfurococaceae; Aeropyrum.  
 OX NCBI\_TaxID=56636;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K1;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Maikawa Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anka H., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Maeda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix K1.";  
 RL DNA Res. 6:83-101(1999).  
 DR EMBL; AP000062; BAA80676.1; -.  
 DR PIR; G72548; G72548.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 155 AA; 16841 MW; 1AA47C685D52939B CRC64;  
  
 Query Match 2.5%; Score 7; DB 2; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 135 TLSSPNS 141  
 Db 88 TLSSPNS 94  
 |||||  
 |||||  
  
 RESULT 32  
 Q83TU1  
 ID Q83TU1 PRELIMINARY; PRT; 157 AA.  
 AC Q83TU1;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Newman; and ISP479C;  
 RX MEDLINE=22925846; PubMed=14563862;  
 RX DOI=10.1128/JB.185.21.6278-6286.2003;  
 RA Steinhuber A., Goerke C., Bayer M.G., Doring G., Wolz C.;  
 RT "Molecular architecture of the regulatory locus eae of Staphylococcus  
 RT aureus and its impact on the expression of virulence factors.";  
 RL J. Bacteriol. 185:6278-6286(2003).  
 DR EMBL; AJ556794; CAD89109.1; -.  
 DR EMBL; AJ556795; CAD89113.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 157 AA; 17665 MW; AF973D8D9D5D5963E CRC64;

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Query Match      2.5%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
Db 90 ASFFGAF 96

RESULT 33
Q6GBC3 PRELIMINARY; PRT; 157 AA.
ID Q6GBC3
AC Q6GBC3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN OrderedLocusNames=SA0672;
OS Staphylococcus aureus (strain MSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG42448.1; -.
KW Complete proteome.
SQ SEQUENCE 157 AA; 17665 MW; AF973D8D95D5963E CRC64;

Query Match      2.5%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
Db 90 ASFFGAF 96

RESULT 34
Q6GIT5 PRELIMINARY; PRT; 157 AA.
ID Q6GIT5
AC Q6GIT5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN OrderedLocusNames=SA0760;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;

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RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG39770.1; -.
KW Complete proteome.
SQ SEQUENCE 157 AA; 17665 MW; AF973D8D95D5963E CRC64;

Query Match      2.5%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
Db 90 ASFFGAF 96

RESULT 35
Q9N8D4 PRELIMINARY; PRT; 172 AA.
ID Q9N8D4
AC Q9N8D4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acetyltransferase, possible.
GN Name=Tb927.1.4490;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Berriman M., Lennard N.J., Harris B.R., Hertz-Fowler C.,
RA Bart-Delabesse E.N., Gerrard C.S., Atkin R.J., Barron A.J., Bowman S.,
RA Bray-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
RA Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper A.D.,
RA Kay M.P., Leech V., Mayes R., Price C., Quail M.A., Rabinowitch E.,
RA Reitter C., Rutherford K., Sasse J., Sharp S., Showkeen R.,
RA Macleod A., Taylor S., Tweedie A., Turner C.M.R., Tait A., Gull K.,
RA Barrell B., Melville S.E.;
RT "The DNA sequence of chromosome I of an African trypanosome: gene
RT content, chromosome organisation, recombination and polymorphism.";
RL Nucleic Acids Res. 31:4864-4873(2003).
DR EMBL; AL929607; F8N5609.1; -.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1;
KW Transferase.
SQ SEQUENCE 172 AA; 19682 MW; B5DD1A59A77E2AB9 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 NSKNEKA 146
Db 142 NSKNEKA 148

RESULT 36
Q7R3Y3 PRELIMINARY; PRT; 191 AA.
ID Q7R3Y3
AC Q7R3Y3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GUP 69.61978 62553.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;

```

RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 RA Olsen G.J., Sogin M.L.;  
 RT "Draft sequence of the Giardia lamblia genome.";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AACB01000012; EAA42045.1; --  
 SQ SEQUENCE 191 AA; 21255 MW; FID7FEF8FFCC2A73 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 191;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 ELKQMD 47  
 |||||  
 Db 125 ELKQMD 131

## RESULT 37

YQ05\_XANCP STANDARD; PRT; 193 AA.  
 ID YQ05\_XANCP STANDARD; PRT; 193 AA.

AC Q8P7K6;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Hypothetical UPF0307 protein XCC2605.  
 GN OrderedLocusNames=XCC2605;  
 OS Xanthomonas campestris (pv. campestris).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 CC Xanthomonadaceae; Xanthomonas.  
 CC NCBI\_TaxID=340;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33913 / NCPPB 528;  
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
 RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,  
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RA "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities";  
 RL Nature 417:459-463(2002).

-!- SIMILARITY: Belongs to the UPF0307 family.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AE012372; AAM41877.1; --

DR HAMAP; MF 00765; 1;  
 DR InterPro; IPR006839; DUF615.  
 DR InterPro; IPR001232; Skp1.  
 DR InterPro; IPR008945; Skp1\_Skp2.  
 DR Pfam; PF04751; DUF615; 1.  
 DR PIRSF; PIRSF016183; UCP016183; 1.  
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 193 AA; 22001 MW; F00A357929414027 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRLVR 89  
 |||||  
 Db 138 QLRLVR 144

## RESULT 38

YR66\_XANAC STANDARD; PRT; 193 AA.  
 ID YR66\_XANAC STANDARD; PRT; 193 AA.

AC Q8PIK9;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Hypothetical UPF0307 protein XAC2766.  
 GN OrderedLocusNames=XAC2766;  
 OS Xanthomonas axonopodis (pv. citri).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 CC Xanthomonadaceae; Xanthomonas.  
 CC NCBI\_TaxID=92829;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=306 / ATCC 13902 / XV 101;  
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
 RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,  
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RA "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities";  
 RL Nature 417:459-463(2002).

-!- SIMILARITY: Belongs to the UPF0307 family.

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CC EMBL; AE011917; AAM37611.1; ALT\_INIT.

DR HAMAP; MF 00765; 1;  
 DR InterPro; IPR006839; DUF615.  
 DR InterPro; IPR001232; Skp1.  
 DR InterPro; IPR008945; Skp1\_Skp2.  
 DR Pfam; PF04751; DUF615; 1.  
 DR PIRSF; PIRSF016183; UCP016183; 1.  
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 193 AA; 22033 MW; F3418B2APAP98257 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRLVR 89  
 |||||  
 Db 138 QLRLVR 144

RESULT 39  
 LIPB NITEU STANDARD; PRT; 204 AA.  
 AC Q82UJ6; 2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Lipoyltransferase [EC 2.3.1.-] (Lipoyl-(acyl-carrier protein)-protein  
 DE -N-lipoyltransferase (Lipoate-protein ligase B).  
 GN Name=lipB; OrderedLocuNames=NEI1488;  
 OS Nitrosomonas europaea.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 OC Nitrosomonadaceae; Nitrosomonas.  
 OX NCBI\_TaxID=915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19718 / IFO 14298;  
 RX MEDLINE=22586410; PubMed=12700255;  
 RX DOI=10.1128/JB.185.9.2759-2773.2003;  
 RA Chain P., Lamerdin J.E., Larimer P.W., Regala W., Lao V., Land M.L.,  
 RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
 RA Acierro D.M., Holmes N.G., Whittaker M.M., Arp D.J.;  
 RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
 RT obligate chemolithoautotroph Nitrosomonas europaea.";  
 RL J. Bacteriol. 185:2759-2773(2003).  
 CC -!- FUNCTION: Catalyzes the transfer of the endogenously synthesized  
 CC lipoyl group to apoproteins, creating an amide linkage that joins the  
 CC free carboxyl group of lipoyl acid to the epsilon-amino group of a  
 CC specific lysine residue in lipoyl-dependent enzymes. Utilizes  
 CC lipoyl-acyl-carrier protein as a source of lipoyl groups, although  
 CC octanoyl groups from octanoyl-ACP can also be transferred to the  
 CC lipoyl domain of apoproteins (By similarity).  
 CC -!- CATALYTIC ACTIVITY: lipoyl-(acyl-carrier protein) + apo-protein =  
 CC holo-protein + acyl-carrier protein.  
 CC -!- PATHWAY: Endogenous lipoyl metabolism; lipoylation step.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the lipB family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; BX321861; CAD85399.1; -;  
 DR HAMAP; MF 00013; -; 1.  
 DR InterPro; IPR004143; BPL\_LipA\_LipB.  
 DR InterPro; IPR000544; Lipoyl\_B.  
 DR Pfam; PF03099; BPL\_LipA\_LipB\_1.  
 DR ProDom; PD006086; Lipoyl\_B; 1.  
 DR TIGRFAMs; TIGR00214; lipB; 1.  
 DR PROSITE; PS01313; lipB; 1.  
 DR ACylttransferase; Complete proteome; Transferase.  
 KW ACylttransferase; Complete proteome; Transferase.  
 SQ SEQUENCE 204 AA; 22764 MW; A83F5EF5F0346E61 CRC64;  
 Query Match 2.5%; Score 7; DB 1; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 85 RQLVRKM 91  
 DQ 97 RQLVRKM 103  
 RESULT 40  
 GEMI HUMAN STANDARD; PRT; 209 AA.  
 ID -GEMI\_HUMAN  
 AC Q75436; Q9H121;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT

DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Geminin.  
 GN Name=GMN;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98297356; PubMed=9635433; DOI=10.1016/S0092-8674(00)81209-X;  
 RA McGarry T.J., Kirschner M.W.;  
 RT "Geminin, an inhibitor of DNA replication, is degraded during  
 RT mitosis.";  
 RL Cell 93:1043-1053(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Corby N.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung, and Urinary bladder;  
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Inhibits DNA replication by preventing the incorporation  
 CC of MCM complex into prereplicative complex (pre-RC). It is  
 CC degraded during the mitotic phase of the cell cycle. Its  
 CC destruction at the metaphase-anaphase transition permits  
 CC replication in the succeeding cell cycle.  
 CC -!- DEVELOPMENTAL STAGE: Absent during G1 phase, accumulates during S,  
 CC G2, and M phases, and disappears at the time of the metaphase-  
 CC anaphase transition.  
 CC -!- SIMILARITY: Belongs to the geminin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF067855; AAC39787.1; -;  
 DR EMBL; ALJ13264; CAC21511.1; ALT\_INIT.  
 DR EMBL; BC005185; AAH05185.1; -;  
 DR EMBL; BC005389; AAH05389.1; -;  
 DR IntAct; Q75496; -; GMN.  
 DR Genew; HGNC:17493; GMN.  
 DR H-InvDB; HIX0005629; -;  
 DR Reactome; Q75496; -;  
 DR GO; GO:0007050; P:cell cycle arrest; TAS.  
 DR GO; GO:0008156; P:negative regulation of DNA replication; TAS.  
 DR InterPro; IPR009984; Geminin.  
 DR Pfam; PF07412; Geminin; 1.  
 KW Cell cycle.

```
SQ SEQUENCE 209 AA; 23565 MW; 0BABE60F6F5AC252 CRC64;
Query Match 2.5%; Score 7; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
Db 9 QEEIKEN 15

RESULT 41
Q9LTD0 PRELIMINARY; PRT; 217 AA.
ID Q9LTD0
AC Q9LTD0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE HR-like lesion-inducing protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025608; BAA95731.1; -.
DR InterPro; IPR008637; HR lesion.
DR InterPro; IPR011592; Surf4 rel.
PFam; PF05514; HR lesion; 1.
DR ProDom; PD010195; Surf4 rel; 1.
SQ SEQUENCE 217 AA; 25219 MW; F88CDE1A0BEABC4F CRC64;

Query Match 2.5%; Score 7; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 SPFGAFL 279
Db 88 SPFGAFL 94

RESULT 42
Q6S8A0 PRELIMINARY; PRT; 220 AA.
ID Q6S8A0
AC Q6S8A0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE P1B-type ATPase (Fragment).
OS Acidovorax sp. B0447.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Acidovorax.
OX NCBI_TaxID=263568;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B0447;
RX PubMed=15006795; DOI=10.1128/AEM.70.3.1698-1707.2004;
RA Coombs J.M., Barkay T.;
RT "Molecular evidence for the evolution of metal homeostasis genes by
RT lateral gene transfer in bacteria from the deep terrestrial
RT subsurface.";
RL Appl. Environ. Microbiol. 70:1698-1707(2004).
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DR EMBL; AY463186; AAS19962.1; -.
DR InterPro; IPR001757; ATPase_EI-E2.
DR InterPro; IPR005834; Dehalo_Like_Hydro.
DR Pfam; PF00702; Hydrolase; 1.
DR PROSITE; PS00154; ATPASE_EI_E2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 220
SQ SEQUENCE 220 AA; 23104 MW; 45AC3A0F411769FE CRC64;

Query Match 2.5%; Score 7; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 ELVIHEK 179
Db 126 ELVIHEK 132

RESULT 43
Q89V44 PRELIMINARY; PRT; 220 AA.
ID Q89V44
AC Q89V44;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE B1r1214 protein.
GN OrderedLocusNames=blr1214;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005939; BAC46479.1; -.
KW Complete proteome.
SQ SEQUENCE 220 AA; 23332 MW; 0AD03221F4C1A350 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 LVREGRP 119
Db 110 LVREGRP 116

RESULT 44
Q7MMP6 PRELIMINARY; PRT; 222 AA.
ID Q7MMP6
AC Q7MMP6;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein VV1021.
GN OrderedLocusNames=VV1021;
OS Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Li J.-C., Su T.-L.,
```

RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;  
 RT "Comparative genome analysis of *Vibrio vulnificus*, a marine  
 pathogen."  
 RL Genome Res. 13:2577-2587(2003).  
 DR EMBL: AP005334; BAC93785.1; -;  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 222 AA; 24807 MW; 94A0EF9F43F33FAD CRC64;

Query Match 2.5%; Score 7; DB 2; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GIFEKKE 252  
 |||||  
 Db 190 GIFEKKE 196

## RESULT 45

ID Q8DFN8 PRELIMINARY; PRT; 222 AA.  
 AC Q8DFN8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Uncharacterized protein conserved in bacteria.  
 GN OrderedLocusNames=VV10168;  
 OS *Vibrio vulnificus*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; *Vibrio*.  
 OX NCBI\_TaxID=672;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=CMCP6;  
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
 RA Choy H.E.;  
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6."  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE016797; AAO08706.1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 222 AA; 24807 MW; 94A0EF9F43F33FAD CRC64;

Query Match 2.5%; Score 7; DB 2; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GIFEKKE 252  
 |||||  
 Db 190 GIFEKKE 196

## RESULT 46

ID Q72XY8 PRELIMINARY; PRT; 230 AA.  
 AC Q72XY8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Membrane protein, putative.  
 GN OrderedLocusNames=BCE5235.  
 OS *Bacillus cereus* (strain ATCC 10987).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 OX NCBI\_TaxID=222523;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP PubMed=14960714; DOI=10.1093/nar/gkh258;  
 RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,  
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,  
 RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;  
 RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic  
 adaptations and a large plasmid related to *Bacillus anthracis* pX01."  
 RL Nucleic Acids Res. 32:977-988(2004).  
 DR EMBL: AE017280; AAS44136.1; -;  
 DR TIGR: BCE5235; -;

DR GO: 0016020; C:membrane; IEA.  
 DR InterPro: IPR007300; LrgB.  
 DR Pfam: PF04172; LrgB; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 230 AA; 24443 MW; 189C4651DAE35A72 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 VIETVLL 26  
 |||||  
 Db 11 VIETVLL 17

## RESULT 47

ID P90611 PRELIMINARY; PRT; 231 AA.  
 AC P90611;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE H4 protein.  
 OS *Toxoplasma gondii*.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;  
 OC Toxoplasma.  
 OX NCBI\_TaxID=5811;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BK;  
 RX MEDLINE=20542029; PubMed=11087916; DOI=10.1016/S0166-6851(00)00296-6;  
 RA Brydges S.D., Sherman G.D., Nockemann S., Loyens A., Daubener W.,  
 RA Drenth J.F., Curruhera V.B.;  
 RT "Molecular characterization of IgM1C5, a proteolytically processed  
 antigen secreted from the micronemes of *Toxoplasma gondii*."  
 RL Mol. Biochem. Parasitol. 111:151-66(2000).  
 DR EMBL: Y09782; CAA70921.1; -;  
 SQ SEQUENCE 231 AA; 25984 MW; 9C5B084690B36314 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 FQBEIKE 198  
 |||||  
 Db 137 FQBEIKE 143

## RESULT 48

ID Q7PY53 PRELIMINARY; PRT; 232 AA.  
 AC Q7PY53;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE AGCP12066.  
 GN Names=agCG47164; ORFNames=ENSANGG00000006384;  
 OS *Anopheles gambiae* str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; *Anopheles*.  
 OX NCBI\_TaxID=180454;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=PEST;  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL: AAA0100987; EAA01660.1; -;  
 SQ SEQUENCE 232 AA; 25104 MW; C0C96A97FB332E0B CRC64;

Query Match 2.5%; Score 7; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 TVLQSL 29  
Db 46 TVLQSL 52

RESULT 49

Q5983 PRELIMINARY; PRT; 232 AA.

AC Q6S9B3  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE PIB-type ATPase (fragment).  
OS Acidovorax sp. B0054.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Comamonadaceae; Acidovorax.  
OX NCBI\_TaxID=263555;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B0054;  
RX PubMed=15006795; DOI=10.1128/AEM.70.3.1698-1707.2004;  
RA Coombs J.M., Barkay T.;  
RT "Molecular evidence for the evolution of metal homeostasis genes by lateral gene transfer in bacteria from the deep terrestrial subsurface.";  
RL Appl. Environ. Microbiol. 70:1698-1707(2004).  
DR EMBL; AY463173; AAS19949.1; -;  
DR GO; GO:0003824; P:catalytic activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR001757; ATPase\_E1-E2.  
DR InterPro; IPR008250; E1-E2\_ATPase\_reg.  
DR Pfam; PF00122; E1-E2\_ATPase; 1.  
DR PROSITE; PS00154; ATPASE\_E1\_E2; UNKNOWN\_1.  
FT NON\_TER 1  
FT NON\_TER 232  
SQ SEQUENCE 232 AA; 24249 MW; F85D924477FB916F CRC64;

Query Match 2.5%; Score 7; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 ELVIHEK 179  
Db 139 ELVIHEK 145

RESULT 50

CD7\_HUMAN  
ID - CD7\_HUMAN  
AC P09564;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE T-cell antigen CD7 precursor (GP40) (T-cell leukemia antigen) (TP41) (Leu-9).  
GN Name=CD7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88111517; PubMed=3501369;  
RA Aruffo A., Seed B.;  
RT "Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell expression system.";  
RL EMBO J. 6:3313-3316(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91110576; PubMed=1703303;

RA Schanberg L.E., Fleenor D.E., Kurtzberg J., Haynes B.F., Kaufman R.E.;  
RT "Isolation and characterization of the genomic human CD7 gene; structural similarity with the murine Thy-1 gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:603-607(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP SEQUENCE OF 205-240 FROM N.A.  
RX MEDLINE=91267564; PubMed=1711009;  
RA Yoshikawa K., Seto M., Ueda R., Obata Y., Notake K., Yokochi T.,  
RA Takahashi T.;  
RT "Molecular cloning of the gene coding for the human T cell differentiation antigen CD7.";  
RL Immunogenetics 33:352-360(1991).  
RN [5]  
RP TOPOLOGY.  
RX MEDLINE=90063052; PubMed=2479685;  
RA Ware R.E., Searce R.M., Dietz M.A., Starmer C.F., Palker T.J.,  
RA Haynes B.F.;  
RT "Characterization of the surface topography and putative tertiary structure of the human CD7 molecule.";  
RL J. Immunol. 143:3632-3640(1989).  
RN [6]  
RP INTERACTION WITH SECTM1.  
RX MEDLINE=20119303; PubMed=10652336; DOI=10.1074/jbc.275.5.3431;  
RA Lyman S.D., Rocabar S., Rousseau A.-M., Armetrong A., Fanslow W.C.;  
RT "Identification of CD7 as a cognate of the human K12 (SECTM1) protein.";  
RL J. Biol. Chem. 275:3431-3437(2000).  
CC -!- FUNCTION: Not yet known.  
CC -!- SUBUNIT: Interacts with SECTM1.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD7 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd7.htm".  
CC -----  
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CC -----  
CC EMBL; X06180; CAA29546.1; -;  
DR EMBL; M37271; AAA51953.1; -;  
DR EMBL; BC009293; AAH09293.1; -;  
DR EMBL; BC013297; AAH13297.1; -;  
DR EMBL; D00749; BAA00646.1; -;  
DR EMBL; D00747; BAA00646.1; JOINED.  
DR EMBL; D00748; BAA00646.1; JOINED.



```
DR PIR; A39016; A39016.
DR HSSP; P01607; 1BW.
DR Genew; HGNC:1695; CD7.
DR H-InvDB; HIX0014252; -.
DR MIM; 186820; -.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR GO; GO:0005624; C: membrane fraction; TAS.
DR GO; GO:0005886; C: plasma membrane; TAS.
DR GO; GO:0004872; F: receptor activity; TAS.
DR GO; GO:0006955; P: immune response; TAS.
DR GO; GO:0042110; P: T-cell activation; TAS.
DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Antigen; Glycoprotein; Immune response; Immunoglobulin domain;
KW Lipoprotein; Palmitate; Receptor; Repeat; Signal; T-cell;
KW Transmembrane.
FT SIGNAL 1 25 T-cell antigen CD7.
FT CHAIN 26 240 Extracellular (Probable).
FT DOMAIN 181 201 Probable.
FT TRANSMEM 202 240 Cytoplasmic (Probable).
FT DOMAIN 26 130 Ig-like.
FT DOMAIN 145 180 4 X 9 AA tandem repeats, potential spacer
function.
FT DISULFID 35 142 Potential.
FT DISULFID 48 114 Potential.
FT LIPID 198 198 S-palmitoyl cysteine.
FT CARBOHYD 45 45 N-linked (GlcNAc. .).
FT CARBOHYD 96 96 N-linked (GlcNAc. .).
FT REPEAT 145 153 1.
FT REPEAT 154 162 2.
FT REPEAT 163 171 3.
FT REPEAT 172 180 4.
FT REPEAT 180 180 4.
SQ SEQUENCE 240 AA; 25409 MW; EBBCE08279552108 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 134 NTLSPN 140
Db 231 NTLSPN 237

RESULT 51
O64MD3 PRELIMINARY; PRT; 240 AA.
AC O64MD3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=BFP0027;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR EMBL; AP006842; BAD51354.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 240 AA; 27646 MW; DC1CF4292674BEF8 CRC64;
```

```
Query Match 2.5%; Score 7; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 169 LRNGELV 175

Db 101 LRNGELV 107

RESULT 52

ID Q9EZK4 PRELIMINARY; PRT; 247 AA.

AC Q9EZK4;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Rot-like protein Rip.

GN Name=rlp;

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI\_TaxID=1280;

RN [1]

RP SEQUENCE FROM N.A.

RA McNamara P.J., Milligan-Monroe K., Proctor R.A.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF288788; AAG45334.2; -.
DR HSSP; Q53777; 1FZP

DR InterPro; IPR010166; Staph reg Sar.

DR InterPro; IPR009058; Wing\_Hlx\_DNA\_bnd.

DR TIGRFAMS; TIGR01889; Staph reg Sar; 2.

SQ SEQUENCE 247 AA; 29792 MW; D078366866F60B2B CRC64;

Query Match 2.5%; Score 7; DB 2; Length 247;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 255 RIFVSVT 261

Db 91 RIFVSVT 97

RESULT 53

O99RD5

ID O99RD5 PRELIMINARY; PRT; 247 AA.

AC O99RD5;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Staphylococcal accessory regulator A homolog.

GN Name=sarH2; OrderedLocNames=SAV2499;

OS Staphylococcus aureus (strain Mu50 / ATCC 700699).

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI\_TaxID=158878;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MU50 / ATCC 700699;

RE MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matsumaru K., Maruyama A., Murakami H., Hoshoyama A.,

RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RT "Whole genome sequencing of methicillin-resistant Staphylococcus

RT aureus.";

RL Lancet 357:1225-1240(2001).

DR EMBL; AP003365; BAB58661.1; --

DR PIR; D90053; D90053.

DR HSSP; Q53777; 1FZP.

DR InterPro; IPR010166; Staph reg Sar.

DR InterPro; IPR009058; Wing\_Hlx\_DNA\_bnd.



```

DR  TIGRFAMs; TIGR01889; Staph_reg_Sar; 2.
KW  Complete proteome.
SQ  SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
DB 91 RIFVSVT 97

RESULT 54
Q7A004 PRELIMINARY; PRT; 247 AA.
AC Q7A004;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE SarH2 protein.
GN Name=sarH2; OrderedLocusNames=MW2418;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004830; BAB96283.1; --
DR InterPro; IPR010166; Staph_reg_Sar.
DR InterPro; IPR009058; Wing_Hlx_DNA_bnd.
DR TIGRFAMs; TIGR01889; Staph_reg_Sar; 2.
KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
DB 91 RIFVSVT 97

RESULT 55
Q7A3K0 PRELIMINARY; PRT; 247 AA.
AC Q7A3K0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE SarH2 protein.
GN Name=sarH2; OrderedLocusNames=SA2287;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiramatsu K., Kihara H., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayaishi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003137; BAB43590.1; --
DR InterPro; IPR010166; Staph_reg_Sar.
DR InterPro; IPR009058; Wing_Hlx_DNA_bnd.
DR TIGRFAMs; TIGR01889; Staph_reg_Sar; 2.
KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
DB 91 RIFVSVT 97

RESULT 56
Q6G6H6 PRELIMINARY; PRT; 247 AA.
AC Q6G6H6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Putative staphylococcal accessory regulator.
GN OrderedLocusNames=SA2385;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG44199.1; --
DR InterPro; IPR010166; Staph_reg_Sar.
DR InterPro; IPR009058; Wing_Hlx_DNA_bnd.
DR TIGRFAMs; TIGR01889; Staph_reg_Sar; 2.
KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 247;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
DB 91 RIFVSVT 97

RESULT 57
O94262 PRELIMINARY; PRT; 251 AA.
AC O94262;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE SPBP87.13 protein.
GN Name=SPBP87.13;
OS Schizosaccharomyces pombe (Fision yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

```

OC Schizosaccharomyces.

OX NCBI\_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972h-;

RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,

RA Woodward J., Volktaert G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,

RA Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D.,

RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,

RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Gafteau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RT "The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).

DR EMBL: AL032684; CAA21798.1; --

DR PIR: T40807; T40807

DR GeneDB Spombe: SPBP887.l3; --

SQ SEQUENCE 251 AA; 27746 MW; C631E344FDC0D686 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 DPNDDES 72

Db 73 DPNDDES 79

RESULT 58

Q98D64

ID Q98D64

AC Q98D64; PRELIMINARY; PRT; 253 AA.

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE M14839 protein.

GN Rhizobium loti (Mesorhizobium loti).

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI\_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

Mesorhizobium loti";

DNA Res. 7:331-338(2000).

DR EMBL: AP003005; BAB51407.1; --

DR InterPro; IPR000160; GGDEF.

DR Pfam; PF00990; GGDEF; 1.

DR SMART; SMO0267; DUFL; 1.

DR TIGRFAMs; TIGR00254; GGDEF; 1.

DR PROSITE; PS08887; GGDEF; 1.

SQ Complete proteome.

KW SEQUENCE 253 AA; 27656 MW; 358A4F06B9B6C8E CRC64;

Query Match 2.5%; Score 7; DB 2; Length 253;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 FGAFVLVG 281

Db 168 FGAFVLVG 174

RESULT 59

Q636T1

ID Q636T1

AC Q636T1; PRELIMINARY; PRT; 271 AA.

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hydrolase, alpha/beta fold family (EC 3.7.1.-).

GN ORFNames=BTZK3504;

OS Bacillus cereus ZK.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=288681;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ZK;

RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,

RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,

RA Richardson P., Rubin E., Tice H., Tice H.,

RT "Complete genome sequence of Bacillus cereus ZK.";

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: CP000001; AAU16762.1; --

KW Hydrolase.

SQ SEQUENCE 271 AA; 31281 MW; 85C92D54129184BE CRC64;

Query Match 2.5%; Score 7; DB 2; Length 271;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 RFQEEIK 197

Db 170 RFQEEIK 176

RESULT 60

Q81WU0

ID Q81WU0

AC Q81WU0; Q6HUZ3; Q6KP68; PRELIMINARY; PRT; 271 AA.

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hydrolase, alpha/beta fold family.

GN OrderedLocustNames=BA3877, BA39592, GBAA3877;

OS Bacillus anthracis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1392;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Anes / isolate Porton;

RX MEDLINE=22608414; PubMed=12711629; DOI=10.1038/nature01586;

RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,

RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,

RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,

RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

RA Benton J.D., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,  
RA Salzberg S.L., Thomson B., Friedlander A.M., Kohler T.M.,  
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;  
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to  
RT closely related bacteria.";  
RL Nature 423:81-86(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ames / isolate 0581;  
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,  
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,  
RA Fraser C.M.;  
RT "Bacillus anthracis comparative genomics.";  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sterne;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AEO17036; AAP27611.1; -;  
DR EMBL; AEO17334; AAT32991.1; -;  
DR EMBL; AEO17225; AAT55896.1; -;  
DR TIGR; BA3877; -;  
DR TIGR; GBA43877; -;  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:006725; P:aromatic compound metabolism; IEA.  
DR InterPro; IPR000073; A/b hydrolase.  
DR InterPro; IPR003089; AB hydrolase.  
DR InterPro; IPR000379; Ser\_estr.  
DR Pfam; PF00561; Abhydrolase\_1; i.  
DR PRINTS; PR00111; ABHYDROLASE.  
KW Complete proteome; Hydrolase.  
SQ SEQUENCE 271 AA; 31338 MW; D01E8F4D025FF187 CRC64;  
  
Query Match 2.5%; Score 7; DB 2; Length 271;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
  
QY 191 RFQEEIK 197  
Db 170 RFQEEIK 176  
[1]|||||  
  
RESULT 61  
ID Q6HF64 PRELIMINARY; PRT; 271 AA.  
AC Q6HF64;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hydrolase, alpha/beta fold family (EC 3.7.1.-).  
GN OrderedLocusNames=BT9727\_3492; konkukian).  
OS *Bacillus thuringiensis* (subsp. konkukian).  
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=180856;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97-27;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RT "Complete genome sequence of *Bacillus thuringiensis* 97-27.";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AEO17355; AAT60562.1; -;  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:006725; P:aromatic compound metabolism; IEA.  
DR InterPro; IPR000073; A/b hydrolase.  
DR InterPro; IPR003089; AB hydrolase.  
DR Pfam; PF00561; Abhydrolase\_1; i.  
DR PRINTS; PR00111; ABHYDROLASE.

KW Complete proteome.  
SQ SEQUENCE 271 AA; 31382 MW; 8E6769086609B7F3 CRC64;  
  
Query Match 2.5%; Score 7; DB 2; Length 271;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
  
QY 191 RFQEEIK 197  
Db 170 RFQEEIK 176  
[1]|||||  
  
RESULT 62  
ID Q8ROLO PRELIMINARY; PRT; 293 AA.  
AC Q8ROLO;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE BC026645 protein (fragment).  
GN Name=BC026645;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC026645; AAH26645.1; -;  
DR MGD; MGI:2446129; BC026645.  
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 93 LRTSEET 99  
Db 5 LRTSEET 11  
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RESULT 63  
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AC Q823E7;  
DT 05-JUL-2004 (rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DE 25-OCT-2004 (Rel. 45, Last annotation update)  
 GN Name=lgf; OrderedLocusNames=CCA00471;  
 OS Chlamydomophila caviae.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.  
 OX NCBI\_TaxID=83557;  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN=GPIC;  
 RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gk321;  
 RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,  
 RA Heidelberg J.F., Holtzapple E.K., Khouri H.M., Fedorova N.B.,  
 RA Carty H.A., Unayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,  
 RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,  
 RA Bavoil P.M., Fraser C.M.;  
 RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):  
 examining the role of niche-specific genes in the evolution of the  
 Chlamydiaceae.";  
 RL Nucleic Acids Res. 31:2134-2147(2003).  
 CC -!- FUNCTION: Transfers the N-acyl diglyceride group on what will  
 become the N-terminal cysteine of membrane lipoproteins (By  
 similarity).  
 CC -!- PATHWAY: Lipoprotein biosynthesis; first step.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 (Probable).  
 CC -!- SIMILARITY: Belongs to the lgt family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
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 DR HAMAP; MF 01147; -; 1.  
 DR InterPro; IPR001640; LGT.  
 DR Pfam; PF01790; LGT; 1.  
 DR TIGRFAMs; TIGR00544; lgt; 1.  
 DR PROSITE; PS01311; LGT; FALSE NEG.  
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 FT TRANSMEM 26 48 Potential.  
 FT TRANSMEM 69 91 Potential.  
 FT TRANSMEM 111 130 Potential.  
 FT TRANSMEM 137 159 Potential.  
 FT TRANSMEM 194 216 Potential.  
 FT TRANSMEM 223 245 Potential.  
 FT TRANSMEM 260 282 Potential.  
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 DB 278 GIACFLK 284  
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 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Membrane protein, putative.  
 GN OrderedLocusNames=SAG1731;  
 OS Streptococcus agalactiae (serotype V).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.  
 OX NCBI\_TaxID=216466;  
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 RC STRAIN=2603 V/R / Serotype V;  
 RX MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;  
 RA Tettelin H., Masiognani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,  
 RA Wesels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,  
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,  
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,  
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,  
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,  
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,  
 RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,  
 RA Fraser C.M.;  
 RT "Complete genome sequence and comparative genomic analysis of an  
 emerging human pathogen, serotype V Streptococcus agalactiae.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).  
 DR EMBL; AEO14270; AAN00594.1; -.  
 DR TIGR; SAG1731; -.  
 KW Complete proteome.  
 SQ SEQUENCE 298 AA; 32410 MW; EAF7720189133FDE CRC64;  
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 DB 92 VLLQSLC 98  
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 AC Q8E3I3;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein gbs1776.  
 GN OrderedLocusNames=gbs1776;  
 OS Streptococcus agalactiae (serotype III).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=216495;  
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 RC STRAIN=NEM316 / Serotype III;  
 RX MEDLINE=22242508; PubMed=12354221;  
 RA Glaeser P., Ruñiok C., Buchrieser C., Chevalier F., Frangeul L.,  
 RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,  
 RA Kunst F.;  
 RT "Genome sequence of Streptococcus agalactiae, a pathogen causing  
 invasive neonatal disease.";  
 RL Mol. Microbiol. 45:1499-1513(2002).  
 DR EMBL; AL766853; CAD47435.1; -.  
 DR Sagalists; gbs1776; -.  
 KW Complete proteome.  
 SQ SEQUENCE 298 AA; 32452 MW; 5BF7720198133368 CRC64;  
 Query Match 2.5%; Score 7; DB 2; Length 298;  
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 DB 92 VLLQSLC 98  
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 ID Q6KZP1  
 AC Q6KZP1;



AC Q9VI33;  
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 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE GN Q92336-PA (AT025555p).  
 DE ORFNames=CG2336;  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
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 OC Ephydroidea; Drosophilidae; Drosophila.  
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 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
 RA Fessler K.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclele J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yao Q.A., Ye J.,  
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhou X., Zhu S., Smith H.O.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Konnoller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Paclele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun. Release 3 of the *Drosophila*  
 RT *melanogaster* euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Konnoller B., Carlson J., Svirskaas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a Genomics perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.B., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 [7]  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Paclele J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB003674; AAF54111.4; -;  
 DR EMBL; AY089235; AAL89973.1; -;  
 DR IntAct; Q9VI33; -;  
 DR FlyBase; FBGN0037455; CG2336.  
 DR InterPro; IPR009961; DUF1487.  
 DR Pfam; PF07368; DUF1487; 1.  
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 Db 16 VOYIYKY 22  
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 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=Xf0992;  
 OS *Xylella fastidiosa*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xylella.  
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 RC STRAIN=9a5c;  
 RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;  
 RA Simpson A.J.G., Reinach F.C., Aruda P., Abreu P.A., Acencio M.,  
 RA Alvares R., Alves L.M.C., Araya J.E., Bata G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
 RA Coutinho N.B., Colombo C., Costa F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,  
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
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RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
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RA Menck C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,  
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
RA de Souza A.P., Terenzi M.P., Truffi D., Teai S.M., Tsubako M.H.,  
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
RA Zago M.A., Zatz M., Maidanis J., Setubal J.C.,  
RT "The genome sequence of the plant pathogen *Xylella fastidiosa*,"  
RL Nature 406:151-159(2000).  
DR ENBL; AE003937; AAF83802.1; --  
DR PIR; H82736; H82736.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR InterPro; IPR000379; Ser esters.  
KW Complete proteome; Hypothetical protein.  
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DB 164 SPLVRER 170  
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DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE ADP-L-GLYCERO-D-MANNONHEPTOSE-6-EPIMERASE.  
GN Name-gmh; OrderedLocusNames=JHP0793;  
OS Helicobacter pylori J99 (Campylobacter pylori J99).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=85963;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;  
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
RA Trust T.J.,  
RT "Genomic sequence comparison of two unrelated isolates of the human  
RT gastric pathogen *Helicobacter pylori*,"  
RL Nature 397:176-180(1999).  
DR ENBL; AE001509; AAD06369.1; --  
DR PIR; D71887; D71887.  
DR HSSP; P14169; IORR.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.  
DR InterPro; IPR001509; Epimerase\_Dh.  
DR Pfam; PF01370; Epimerase; 1.  
KW Complete proteome.  
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QY 132 RSNLTSS 138  
DB 46 RSNLTSS 52  
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ID Q7VJZ3 PRELIMINARY; PRT; 343 AA.  
AC Q7VJZ3  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE DTDp-D-glucose 4,6-dehydratase (EC 4.2.1.46).  
GN OrderedLocusNames=HH0099;  
OS Helicobacter hepaticus.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=32025;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 51449 / 3B1;  
RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;  
RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,  
RA Bell M., Droege M., Partmann B., Fischer H.-P., Ge Z., Hoerster A.,  
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,  
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.,  
RT "The complete genome sequence of the carcinogenic bacterium  
RT Helicobacter hepaticus,"  
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).  
CC -1- SIMILARITY: Belongs to the sugar epimerase family.  
DR ENBL; AE017144; AAP76696.1; --  
DR HSSP; P27830; IBXK.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0008460; F:DTDp-glucose 4,6-dehydratase activity; IEA.  
DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.  
DR InterPro; IPR005888; DTDp Gluc dehyd.  
DR InterPro; IPR001509; Epimerase\_Dh.  
DR Pfam; PF01370; Epimerase; 1.  
DR TIGRfam; TIGR01181; DTDp Gluc dehyd; 1.  
KW Complete proteome; NAD.  
SQ SEQUENCE 343 AA; 38920 MW; B528F6F2710A40D2 CRC64;  
Query Match 2.5%; Score 7; DB 2; Length 343;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
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QY 209 YIYKTS 215  
DB 329 YIYKTS 335  
RESULT 73  
O84846  
ID O84846 PRELIMINARY; PRT; 354 AA.  
AC O84846  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein CT839.  
GN OrderedLocusNames=CT839;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D / UW-3 / Cx;  
RX MEDLINE=99000809; PubMed=9784136; DOI=10.1126/science.282.5389.754;  
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,  
RA Davis R.W.,  
RT "Genome sequence of an obligate intracellular pathogen of humans:  
RT Chlamydia trachomatis,"  
RL Science 282:754-759(1998).



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DR EMBL; AE001356; AAC68436.1; -.
DR PIR; G71465; G71465.
DR GO; GO:0016021; C-integral to membrane; IEA.
DR InterPro; IPR005495; Yjgp_YjgQ.
DR Pfam; PF03739; Yjgp_YjgQ; 1.
KW Complete proteome.
SQ SEQUENCE 354 AA; 40065 MW; AD79C8F2CD59F4E5 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
DB 150 KENDRIF 156
|||||

RESULT 74
Q9PL80 PRELIMINARY; PRT; 354 AA.
AC Q9PL80;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein TC0227.
GN OrderedLocusNames=TC0227;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
ON NCBI_TaxID=83560;
RX STRAIN=MOpn / Nigg;
RC MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwin M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MOpn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406 (2000).
DR EMBL; AE002289; AAF39099.1; -.
DR PIR; A81728; A81728.
DR TIGR; TC0227; -.
DR GO; GO:0016021; C-integral to membrane; IEA.
DR InterPro; IPR005495; Yjgp_YjgQ.
DR Pfam; PF03739; Yjgp_YjgQ; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 354 AA; 40145 MW; E6A1317A124C10D1 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
DB 150 KENDRIF 156
|||||

RESULT 75
Q9AVE6 PRELIMINARY; PRT; 359 AA.
AC Q9AVE6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE OSTATC protein.
GN Names=OSTATC; Synonyms=B1080D07.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
ON NCBI_TaxID=39947;

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RN SEQUENCE FROM N.A.
RP MEDLINE=21140310; PubMed=11244106; DOI=10.1104/pp.125.3.1248;
RX Agrawal G.K., Yamazaki M., Kobayashi M., Hirochika R., Miyao A.,
RA Hirochika H.;
RT "Screening of the rice viviparous mutants generated by endogenous
RT retrotransposon Tos17 insertion. Tagging of a zeaxanthin epoxidase
RT gene and a novel ostac gene."
RL Plant Physiol. 125:1248-1257 (2001).
RN [2]
SQ SEQUENCE FROM N.A.
RP PubMed=12447438; DOI=10.1038/nature01184;
RX Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K. Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1."
RL Nature 420:312-316 (2002).
DR EMBL; AB050885; BAB39766.1; -.
DR EMBL; AP003203; BAB64068.1; -.
DR Gramene; Q9AVE6; -.
DR InterPro; IPR002033; Translocase.
DR Pfam; PF0902; TatC; 1.
DR PRINTS; PR01840; TATCFAMILY.
DR TIGRPFAM; TIGR00945; tatC; 1.
DR PROSITE; PS01218; TATC; 1.
SQ SEQUENCE 359 AA; 38763 MW; D25349B32FE1B540 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 DRIFSV 260
DB 141 DRIFSV 147
|||||

Search completed: June 22, 2005, 06:51:54
Job time : 183 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:03:21 ; Search time 164 Seconds  
(without alignments)  
662.681 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMVEVQGPGSLGTCVTLIV.....NEHLIDMDHEASFFGAFVLVG 281

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A\_Genesep\_16Dec04.\*

1: Genesep1980s.\*

2: Genesep1990s.\*

3: Genesep2000s.\*

4: Genesep2001s.\*

5: Genesep2002s.\*

6: Genesep2003as.\*

7: Genesep2003bs.\*

8: Genesep2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	281	100.0	281	2	AAW19777	Aaw19777 Novel cyt
2	281	100.0	281	2	AAW27134	Aaw27134 Human Apo
3	281	100.0	281	2	AAW19787	Aaw19787 Human apo
4	281	100.0	281	2	AAW76829	Aaw76829 Human TL2
5	281	100.0	281	2	AAW56760	Aaw56760 Human TRA
6	281	100.0	281	2	AAW44354	Aaw44354 Human AGP
7	281	100.0	281	2	AAW101517	Aaw101517 Protein a
8	281	100.0	281	2	AAW27012	Aaw27012 Human Apo
9	281	100.0	281	3	AAW81956	Aaw81956 Human Apo
10	281	100.0	281	3	AAW24038	Aaw24038 Human PRO
11	281	100.0	281	3	AAW08545	Aaw08545 Amino aci
12	281	100.0	281	3	AAW28691	Aaw28691 Human AGP
13	281	100.0	281	4	AAW50977	Aaw50977 Human PRO
14	281	100.0	281	4	AAW67243	Aaw67243 Human Apo
15	281	100.0	281	4	AAW11031	Aaw11031 Human TNF
16	281	100.0	281	4	AAW48350	Aaw48350 Human TL2
17	281	100.0	281	5	AAW08133	Aaw08133 Human TRA
18	281	100.0	281	5	AAW31630	Aaw31630 Human TRA
19	281	100.0	281	5	AAW50662	Aaw50662 Human TNF
20	281	100.0	281	5	AAW51077	Aaw51077 Human Apo
21	281	100.0	281	5	AAW51954	Aaw51954 Human Apo
22	281	100.0	281	5	AAW19095	Aaw19095 C neofor
23	281	100.0	281	5	AAW79593	Aaw79593 Human TNF
24	281	100.0	281	6	AAW73861	Aaw73861 Human Apo
25	281	100.0	281	6	AAW10205	Aaw10205 Human Apo

26	281	100.0	281	6	ABU71443	Abu71443 Human neo
27	281	100.0	281	6	ABG72738	Abg72738 Human TNF
28	281	100.0	281	6	AAO29543	Aao29543 Human TRA
29	281	100.0	281	6	ABU08558	Abu08558 Human TNF
30	281	100.0	281	6	ABR42313	AbR42313 Human TRA
31	281	100.0	281	6	ABG71905	Abg71905 Human TRA
32	281	100.0	281	6	ABP60546	Abp60546 Human tum
33	281	100.0	281	6	AAE36258	Aae36258 Human TRA
34	281	100.0	281	6	AAO31151	Aao31151 Human TNF
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37	281	100.0	281	7	ADC35202	AdC35202 Human TNF
38	281	100.0	281	7	ADD14080	AdD14080 Human sxc
39	281	100.0	281	7	ADD19010	AdD19010 Human dls
40	281	100.0	281	7	ABW02276	AbW02276 Human TRA
41	281	100.0	281	8	ADE76953	AdE76953 Human pro
42	281	100.0	281	8	ADK72311	AdK72311 Human Apo
43	281	100.0	281	8	ADK72303	AdK72303 Human Apo
44	281	100.0	281	8	ADK72304	AdK72304 Human Apo
45	281	100.0	281	8	ADK72296	AdK72296 Human wll
46	281	100.0	281	8	ADK72310	AdK72310 Human Apo
47	281	100.0	281	8	ADJ63976	AdJ63976 Human apo
48	281	100.0	281	8	ADL71816	AdL71816 Human apo
49	281	100.0	281	8	ADK15498	AdK15498 Human TRA
50	281	100.0	281	8	ADN07587	AdN07587 Human apo
51	281	100.0	281	8	ADR14209	AdR14209 Human NP-
52	281	100.0	281	8	ADK82215	AdK82215 Human TRA
53	281	100.0	281	8	ADS88000	AdS88000 Tumour tr
54	281	100.0	281	8	ABO84415	AbO84415 Human can
55	281	100.0	281	8	ADP23388	AdP23388 PRO polyP
56	280	99.6	280	7	ADN95444	AdN95444 Human BEC
57	279	99.3	279	2	AAW76332	Aaw76332 Human TL2
58	279	99.3	279	2	AAW95032	Aaw95032 Tumour ne
59	268	95.4	281	2	AAW27018	Aaw27018 Human Apo
60	263	93.6	281	7	ADB61495	AdB61495 Human Apo
61	262	93.2	281	7	ADB61494	AdB61494 Human Apo
62	254	90.4	281	7	ADB61493	AdB61493 Human Apo
63	248	88.3	281	7	ADB61492	AdB61492 Human Apo
64	244	86.8	281	2	AAW01516	Aaw01516 Protein a
65	242	86.1	266	4	AAW72935	Aaw72935 OmpA sign
66	233	82.9	281	7	ADB61491	AdB61491 Human Apo
67	217	77.2	281	2	AAW27017	Aaw27017 Human Apo
68	202	71.9	281	2	AAW27019	Aaw27019 Human Apo
69	202	71.9	281	2	AAW27016	Aaw27016 Human Apo
70	199	70.8	281	5	ABG72257	Abg72257 Human tum
71	193	68.7	212	5	AAU99301	Aau99301 Human TRA
72	188	66.9	281	8	ADK72306	AdK72306 Human Apo
73	188	66.9	281	8	ADK72313	AdK72313 Human Apo
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79	187	66.5	253	4	AAE11037	Aae11037 GH-derive
80	187	66.5	253	6	ABU08564	Abu08564 Human Gro
81	187	66.5	253	8	ADK15507	AdK15507 Human TRA
82	187	66.5	256	4	AAE11038	Aae11038 CMV-deriv
83	187	66.5	256	6	ABU08565	Abu08565 CMV sig.
84	187	66.5	256	8	ADK15509	AdK15509 Human cDN
85	187	66.5	391	8	ADP20791	Adp20791 Fusion co
86	187	66.5	450	7	ADP75172	Adp75172 Fusion co
87	187	66.5	461	5	AAO17496	Aao17496 Antibody-
88	187	66.5	480	5	AAO17495	Aao17495 Antibody-
89	187	66.5	614	5	AAO17494	Aao17494 Antibody-
90	186	66.2	441	3	AAW28692	Aaw28692 FC-huAGP-
91	185	65.8	281	7	ADB61476	AdB61476 Human Apo
92	180	64.1	281	7	ADB61480	AdB61480 Human Apo
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94	180	64.1	281	7	ADB61484	AdB61484 Human Apo
95	180	64.1	281	7	ADB61478	AdB61478 Human Apo
96	180	64.1	281	7	ADB61481	AdB61481 Human Apo
97	180	64.1	281	7	ADB61487	AdB61487 Human Apo
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99 180 64.1 281 7 ADB61490 Human Apo  
100 180 64.1 281 7 ADB61477 Human Apo

## ALIGNMENTS

## RESULT 1

AAW19777 standard; protein; 281 AA.

XX AAW19777;

XX 22-SEP-1997 (first entry)

XX Novel cytokine Apo-2 ligand.

XX Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide /note= "Claim 4"

FT Region 1..14

FT Protein /label= Cytoplasmic\_region

FT Region 15..281

FT Protein /note= "Claim 3"

FT Region 15..40

FT Protein /label= Transmembrane\_region

FT Region 41..281

FT Region 41..281

FT Modified-site /label= Extracellular\_region

FT /label= Glycosylation

FT Protein /note= "putative N-linked glycosylation site"

FT Protein 114..281

XX /note= "Claim 1"

PN WO9725428-A1.

XX 17-JUL-1997.

XX 08-JAN-1997; 97WO-US000272.

XX 09-JAN-1996; 96US-00584031.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Chuntharapai A, Kim KJ;

XX WPI; 1997-372867/34.

DR N-PSDB; AAT72796.

XX Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce

XX apoptosis for the treatment of breast and colon cancer.

XX Claim 4; Fig 1a; 72pp; English.

XX A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian

XX cell apoptosis. It is believed to be a member of the tumour necrosis

XX factor cytokine family. Its amino acid sequence was deduced from a cDNA

XX clone (AAW72796) isolated from a human placental cDNA library. Apo-2

XX ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-

XX 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells

XX transformed or transfected with a vector contg. Apo-2 ligand nucleic

XX acid. They can be used to induce apoptosis in mammals and to treat

XX pathological conditions such as cancer (esp. breast or colon cancer) or

XX to raise antibodies useful in diagnostic assays

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDPNDEBSMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIISPLVRERGPQ 120  
DB 61 DDSYWDPNDEBSMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNIISPLVRERGPQ 120

QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDDPILLMKSAARNCSWSKDAEYGLY 240  
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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

## RESULT 2

AAW27134 standard; protein; 281 AA.

XX AAW27134;

XX 02-APR-1998 (first entry)

XX Human Apoptosis inducing molecule-I (AIM-I).

XX Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;

XX tumour necrosis factor ligand superfamily; AIM-I altered expression;

XX neoplasia inhibition; anti-inflammatory agent.

XX Homo sapiens.

XX WO9733899-A1.

XX 18-SEP-1997.

XX 14-MAR-1996; 96WO-US003773.

XX 14-MAR-1996; 96WO-US003773.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM;

XX WPI; 1997-470807/43.

DR N-PSDB; AAT85210.

XX New isolated apoptosis inducing molecule-I - used to develop products for

XX the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft

XX versus host disease or inflammation.

XX Claim 2; Fig 1; 82pp; English.

XX The present sequence represents a human Apoptosis inducing molecule-I

XX (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand

XX superfamily. The products can be used in the diagnosis and treatment of

XX disorders related to under-expression, over-expression or altered

XX expression of AIM-I. AIM-I or agonists can be used for treating

XX autoimmune disorders including systemic lupus erythematosus,

XX immunoproliferative disease lymphadenopathy (IPL),

XX angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,

XX diabetes, and multiple sclerosis, graft versus host disease, to inhibit

XX neoplasia such as tumour cell growth, to treat restenosis, to regulate

XX haematopoiesis in endothelial cell development, to stimulate peripheral

CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be  
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or  
 CC osteoporosis, for preventing graft-host rejection, and as anti-  
 CC inflammatory agents, for treating endotoxic shock or to prevent  
 CC activation of HIV  
 XX  
 XX Sequence 281 AA;  
 Query Match 100.0%; Score 281; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKGIACFLKE 60  
 DB 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKGIACFLKE 60  
 QY 61 DDSYWDPNDEESMNSPCWQVKQLRQVRKMLRTSEETISTVQEKQKNISPLVRERGPO 120  
 DB 61 DDSYWDPNDEESMNSPCWQVKQLRQVRKMLRTSEETISTVQEKQKNISPLVRERGPO 120  
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 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
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 DB 181 FYIYSQTYFRQFEIKENTKNDKQVYIYKTSYPPDPILLMKARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 3  
 ID AAW19787  
 XX AAW19787 standard; protein; 281 AA.  
 AC AAW19787;  
 DT 24-SEP-1997 (first entry)  
 XX Human apoptosis inducer cytokine TRAIL.  
 DE  
 XX Tumour necrosis factor related apoptosis inducing ligand; TRAIL;  
 KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;  
 KW thrombotic microangioplasty; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..18  
 FT Domain /label= Cytoplasmic\_domain  
 FT Domain 19..38  
 FT Domain /label= Transmembrane\_domain  
 FT Domain 39..281  
 FT /label= Extracellular\_domain  
 FT /note= "contains a receptor-binding region"  
 FT Cleavage-site 89..90  
 FT /note= "potential KEX2 protease processing site"  
 FT Modified-site 109..111  
 FT /note= "potential N-glycosylation site"  
 FT Cleavage-site 149..150  
 FT /note= "potential KEX2 protease processing site"  
 XX  
 PN WO9701633-A1.  
 XX  
 PD 16-JAN-1997.  
 XX  
 PD 25-JUN-1996; 96WO-US010895.  
 XX  
 PR 29-JUN-1995; 95US-00496632.  
 PR 01-NOV-1995; 95US-00548360.  
 XX

PA (IMMV ) IMMUNEX CORP.  
 XX Wiley SR, Goodwin RG;  
 XX WPI; 1997-118715/11.  
 DR N-PSDB; AAT72847.  
 XX  
 XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected  
 PT cells - useful for treating thrombotic microangiopathy, cancer and viral  
 PT infection and for use in assays.  
 XX  
 PS Claim 10; Page 43-44; 62pp; English.  
 CC Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)  
 CC (AAW19787) is a novel cytokine that induces apoptosis of certain target  
 CC cells, including cancer cells and virally infected cells. Its amino acid  
 CC sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in  
 CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble  
 CC polypeptides) can be expressed in host cells and used in the treatment of  
 CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or  
 CC to raise antibodies that may be useful for treating thrombotic  
 CC microangiopathies  
 XX  
 XX Sequence 281 AA;  
 Query Match 100.0%; Score 281; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKGIACFLKE 60  
 DB 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSKGIACFLKE 60  
 QY 61 DDSYWDPNDEESMNSPCWQVKQLRQVRKMLRTSEETISTVQEKQKNISPLVRERGPO 120  
 DB 61 DDSYWDPNDEESMNSPCWQVKQLRQVRKMLRTSEETISTVQEKQKNISPLVRERGPO 120  
 QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRQFEIKENTKNDKQVYIYKTSYPPDPILLMKARNSCWSDAEYGLY 240  
 DB 181 FYIYSQTYFRQFEIKENTKNDKQVYIYKTSYPPDPILLMKARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 4  
 ID AAW76829  
 XX AAW76829 standard; protein; 281 AA.  
 AC AAW76829;  
 DT 25-JAN-1999 (first entry)  
 XX Human TL2 protein.  
 DE  
 XX TR6; tumour necrosis factor related receptor; human; treatment; stroke;  
 KW inflammation; arthritis; septicaemia; autoimmune disease; restenosis;  
 KW transplant rejection; infection; ischaemia; brain injury; bone disease;  
 KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;  
 KW AIDS; cancer; atherosclerosis; Alzheimer's disease; TRAIL; TNF;  
 KW TL2. tumour necrosis factor-related apoptosis-inducing ligand.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP870827-A2.  
 XX  
 PD 14-OCT-1998.  
 XX

PF 23-DEC-1997; 97EP-00310562.  
 XX 14-MAR-1997; 97US-0041230P.  
 PR 09-MAY-1997; 97US-00853684.  
 PR 22-AUG-1997; 97US-00916625.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA Deen KC, Young PR;  
 XX WPI; 1998-523156/45.  
 DR N-PSDB; AAV63096.  
 XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding  
 PT polypeptide, antibody, agonist, antagonist, etc.  
 XX Disclosure; Page 32-33; 34pp; English.  
 PS This sequence represents the human tumour necrosis factor (TNF)-related  
 CC receptor, TL2 (also known as tumour necrosis factor-related apoptosis-  
 CC inducing ligand, TRAIL). This protein is used in a method resulting in  
 CC the isolation of the novel human TNF related receptor, TR6. TR6  
 CC polypeptides and polynucleotides can be used in the treatment of chronic  
 CC and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.  
 CC host disease, infection, stroke, ischaemia, acute respiratory disease  
 CC syndrome, reseriosis, brain injury, (acquired autoimmune disease  
 CC syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative  
 CC disorders), atherosclerosis and Alzheimers disease  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 281; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60  
 QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120  
 DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKITSYPPDILLMKSARNCSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKITSYPPDILLMKSARNCSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281  
 RESULT 5  
 AAW56760  
 ID AAW56760 standard; protein; 281 AA.  
 XX AAW56760;  
 AC AAW56760;  
 XX 05-AUG-1998 (first entry)  
 DT Human TRAIL polypeptide.  
 XX Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;  
 KW cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 ,FH

FT Domain 1. .18  
 FT Region /note= "N-terminal cytoplasmic domain"  
 FT 19. .38  
 FT Domain /note= "transmembrane region"  
 FT 39. .281  
 FT Domain /note= "extracellular domain"  
 PN US5763223-A.  
 XX 09-JUN-1998.  
 PD 25-JUN-1996; 96US-00670354.  
 XX 29-JUN-1995; 95US-00496632.  
 PR 01-NOV-1995; 95US-00548368.  
 XX (IMMV ) IMMUNEX CORP.  
 PA Goodwin RG, Wiley SR;  
 XX WPI; 1998-347322/30.  
 DR N-PSDB; AAV29518.  
 XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful  
 FT for producing recombinant polypeptides for research and therapy of  
 PT leukaemia, lymphoma, melanoma and viral infections.  
 XX Claim 1; Col 33-36; 28pp; English.  
 PS This represents a human tumour necrosis factor related apoptosis ligand  
 CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce  
 CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful  
 CC for producing the recombinant TRAIL polypeptides, which may be useful in  
 CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells  
 CC (e.g. to isolate antigens for vaccine development). The polypeptides can  
 CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal  
 CC treatment of blood or bone-marrow), or to treat viral infections  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 281; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60  
 QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120  
 DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRGPQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKITSYPPDILLMKSARNCSKDAEYGLY 240  
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKITSYPPDILLMKSARNCSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281  
 RESULT 6  
 AAW44354  
 ID AAW44354 standard; protein; 281 AA.  
 XX AAW44354;  
 AC AAW44354;  
 XX 28-MAY-1998 (first entry)  
 DT  
 XX

DE Human AGP-1.  
 XX Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;  
 KW bone resorption; haematopoietic disease.  
 XX Homo sapiens.  
 OS WO9746886-A2.  
 PN 11-DEC-1997.  
 XX 06-JUN-1997; 97WO-US009895.  
 XX 07-JUN-1996; 96US-0060562.  
 XX (AMGE-) AMGEN INC.  
 PA Johnson MJ, Simonet WS, Danilenko DM;  
 PI WPI; 1998-042194/04.  
 DR N-PSDB; AAV15295.  
 XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -  
 PT useful for treating inflammation, bone resorption and haematopoietic  
 PT diseases.  
 XX Claim 7; Page 36-37; 54pp; English.  
 PS The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis  
 CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and  
 CC bone resorption. It has the same nucleic acid and amino acid (aa)  
 CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described  
 CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay  
 CC reagents for detecting AGP-1 expression. Nucleic acid complementary to  
 CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are  
 CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus  
 CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or  
 CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,  
 CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat  
 CC haematopoietic diseases associated with reduction in the number of bone  
 CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused  
 CC by disease, injury or exposure to myelosuppressive agents. Host cells,  
 CC transformed with expression vectors containing AGP-1 DNA, are used to  
 CC produce recombinant AGP-1  
 XX Sequence 281 AA;  
 SQ  
 Query Match 100.0%; Score 281; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNKLQMDKYKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNKLQMDKYKSGIACFLKE 60  
 QY 61 DSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKQNISPLVRERGQ 120  
 DB 61 DSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKQNISPLVRERGQ 120  
 QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARSNCSDAEYGLY 240  
 DB 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARSNCSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 RESULT 7

AA01517  
 ID AAY01517 standard; peptide; 281 AA.  
 XX AC AAY01517;  
 XX DT 27-MAY-1999 (first entry)  
 XX DE Protein associated with neurodegenerative and autoimmune diseases.  
 XX KW Neurodegenerative disease; autoimmune disease; inflammatory disease;  
 KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;  
 XX surface receptor; TRAIL protein.  
 OS Homo sapiens.  
 XX PN FR2766713-A1.  
 XX PD 05-FEB-1999.  
 XX PF 04-AUG-1997; 97FR-00010176.  
 XX PR 04-AUG-1997; 97FR-00010176.  
 XX PA (INNR ) BIO MERIEUX.  
 XX PI Rieger F, Belliveau JF, Perron H;  
 XX WPI; 1999-156177/14.  
 XX Use of polypeptide derived from TRAIL protein for diagnosis of  
 PT degenerative disease - autoimmunity and inflammation, also useful in  
 PT prevention or treatment, and similar use of corresponding ligand and  
 PT nucleic acid.  
 XX Claim 2; Page 13; 21pp; French.  
 PS The specification describes the use a polypeptide corresponding to at  
 CC least the primary sequence of part of the present sequence to produce a  
 CC diagnostic, prophylactic or therapeutic composition useful in cases of  
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can  
 CC be used in treatment of neurodegenerative disease, lupus erythematosus,  
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central  
 CC nervous system cells, antigenic and specifically recognise the surface  
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and  
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an  
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific  
 CC receptors, inhibiting formation of natural complex  
 XX Sequence 281 AA;  
 SQ  
 Query Match 100.0%; Score 281; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNKLQMDKYKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNKLQMDKYKSGIACFLKE 60  
 QY 61 DSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKQNISPLVRERGQ 120  
 DB 61 DSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKQNISPLVRERGQ 120  
 QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 DB 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARSNCSDAEYGLY 240  
 DB 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARSNCSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8  
ID AAY27012 standard; protein; 281 AA.  
XX AC AAY27012;  
XX DT 24-SEP-1999 (first entry)  
XX DE Human Apo-2 ligand (Apo-2L) polypeptide.  
XX Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;  
KW lupus; immune-mediated glomerular nephritis; human.  
XX OS Homo sapiens.  
XX PN WO9936535-A1.  
XX PD 22-JUL-1999.  
XX PF 15-JAN-1999; 99WO-US001039.  
XX PR 15-JAN-1998; 98US-00007886.  
XX PR 15-APR-1998; 98US-00060533.  
XX PA (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;  
XX WPI; 1999-444397/37.  
XX DR N-PSDB; AAX86987.  
XX PT A novel cytokine, designated apo-2 ligand, useful for inducing apoptosis  
PT in mammalian cancer cells.  
XX Claim 1; Fig 1A; 86pp; English.  
XX This sequence represents a novel human cytokine, designated Apo-2 ligand  
CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant  
CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer  
CC cells. This is useful for the treatment of cancer. Apo-2L can be used to  
CC induce apoptosis for pathological conditions characterized by decreased  
CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-  
CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid  
CC coding sequence can also be used in quantitative and screening diagnostic  
CC techniques. Anti-Apo-2L antibodies can be used for treating diseases  
CC associated with increased apoptosis  
XX SQ Sequence 281 AA;  
Query Match 100.0%; Score 281; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266; Mismatches 0; Indels 0; Gaps 0;  
Matches 281; Conservative 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60  
Qy 61 DSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
Db 61 DSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSAARNCSKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSAARNCSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
RESULT 9  
ID AAY81956 standard; protein; 281 AA.  
XX AC AAY81956;  
XX DT 10-JUL-2000 (first entry)  
XX DE Human Apo-2 ligand protein sequence.  
XX Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;  
KW therapy; apoptosis; cancer.  
XX OS Homo sapiens.  
XX PN US6046048-A.  
XX PD 04-APR-2000.  
XX PF 08-JAN-1997; 97US-00780496.  
XX PR 09-JAN-1996; 96US-0009755P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Kim KJ, Ashkenazi AJ, Chuntharapai A;  
XX WPI; 2000-282690/24.  
XX DR N-PSDB; AAA07425.  
XX PT New isolated monoclonal antibodies having antigen specificity for Apo-2  
PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo  
PT -2 ligand serum, and for treating diseases associated with increased  
PT apoptosis.  
XX Claim 9; Fig 1a; 46pp; English.  
XX This sequence is the human Apo-2 ligand protein, which is recognised by  
CC monoclonal antibodies produced by the hybridoma cell lines of the  
CC invention. The hybridoma cell lines are deposited under the American Type  
CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258  
CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic  
CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,  
CC tissues, or serum. The antibodies may also be employed as therapeutics.  
CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand  
CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat  
CC pathological conditions or diseases associated with increased apoptosis.  
CC They are also useful for the affinity purification of Apo-2 ligand from  
CC recombinant cell culture or natural sources. The Apo-2 ligand itself may  
CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells  
XX SQ Sequence 281 AA;  
Query Match 100.0%; Score 281; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266; Mismatches 0; Indels 0; Gaps 0;  
Matches 281; Conservative 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYSGIACFLKE 60  
Qy 61 DSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
Db 61 DSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKSAARNCSKDAEYGLY 240

Db	181	FYIYSQTYFRQEI	KENTKNDKQMVQYIYKYTSYDPDILLKKSARNSCWSKDAEYGLY	240	
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281		
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281		
RESULT 10					
AAB24038					
ID	AAB24038 standard; protein; 281 AA.				
XX	AC	AAB24038;			
XX	XX				
DT	25-JAN-2001 (first entry)				
XX	XX				
DE	Human PRO1096 protein sequence SEQ ID NO:51.				
XX	XX				
XX	XX	Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;			
KW	XX	identification; tumorigenesis; anticancer; detection.			
XX	OS	Homo sapiens.			
XX	OS				
PN	WO200053750-A1.				
XX	XX				
PD	14-SEP-2000.				
XX	XX				
PF	02-DEC-1999; 99WO-US028551.				
XX	XX				
XX	XX	08-MAR-1999; 99WO-US005028.			
PR	01-SEP-1999; 99WO-US020111.				
PR	29-OCT-1999; 99US-0162506P.				
PR	30-NOV-1999; 99WO-US028313.				
PR	01-DEC-1999; 99WO-US028634.				
XX	XX				
PA	(GETH ) GENENTECH INC.				
XX	XX				
PI	Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;				
XX	XX				
WPI	2000-594320/56.				
DR	N-PSDB; AAC58120.				
DR					
XX	XX				
PT	Antibodies specific for PRO polypeptides, used to diagnose and inhibit				
PT	the growth of tumors in mammals, and to identify inhibitors of PRO				
PT	polypeptide activity or expression.				
XX	XX				
PS	Claim 61; Fig 36; 226pp; English.				
XX	XX				
CC	The present invention describes an antibody that binds to a human protein				
CC	(I) selected from: PRO1381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;				
CC	PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO1344; PRO4354; PRO4397;				
CC	PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer				
CC	activity and can be used to diagnose tumours in mammals, by detecting				
CC	complex formation when the antibody is contacted with test cells.				
CC	Increased expression of genes encoding (I) can also be detected to				
CC	diagnose tumours. Agents which inhibit the activity of (I), especially				
CC	the antibodies, or an antisense oligonucleotide which hybridises to genes				
CC	encoding (I), can be used to inhibit tumour growth, preferably by				
CC	inducing cell death. Methods from the present invention can be used to				
CC	identify compounds which inhibit the biological activity of (I). AAC58019				
CC	to AAC58102 represent PCR primers and hybridisation probes used in				
CC	examples from the present invention for human PRO sequences. AAC58103 to				
CC	AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and				
CC	protein sequences given in the exemplification of the present invention				
XX	XX				
XX	XX	Sequence 281 AA;			
XX	XX				
Query Match 100.0%; Score 281; DB 3; Length 281;					
Best Local Similarity 100.0%; Pred. No. 2.9e-266;					
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0					
Qy	1	MANMEYQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDQKYSKGIACFLKE			60



Qy	1	MAMMEVQGGPSLGQTCVLIVIFTVLQSLCAVATVYVYFTNELKQMDKYKSGIACFLKE	60
Db	1	MAMMEVQGGPSLGQTCVLIVIFTVLQSLCAVATVYVYFTNELKQMDKYKSGIACFLKE	60
Qy	61	DDSYWDPNDEESMNSPCQVQKWQLRQLRKMLTRTSEETISTVQEKQONISPLVRRGQP	120
Db	61	DDSYWDPNDEESMNSPCQVQKWQLRQLRKMLTRTSEETISTVQEKQONISPLVRRGQP	120
Qy	121	RVAAHITGTRGSRNTLSPNSKVEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG	180
Db	121	RVAAHITGTRGSRNTLSPNSKVEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG	180
Qy	181	FYYIYSQTYFRFQBEIKENTKNDKMVQYIYKYTSYDPDILLMKSGARNCSWKDAEYGLY	240
Db	181	FYYIYSQTYFRFQBEIKENTKNDKMVQYIYKYTSYDPDILLMKSGARNCSWKDAEYGLY	240
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
RESULT 12			
AAB28691			
ID	AAB28691 standard; protein; 281 AA.		
XX	XX		
XX	AC AAB28691;		
XX	XX		
DT	14-FEB-2001 (first entry)		
XX	XX		
DE	Human AGP-1.		
XX	XX		
KW	Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;		
KW	anti-inflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;		
KW	human immunodeficiency virus; apoptosis; proliferative disorder; cancer;		
KW	hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;		
KW	transplant rejection; cardiovascular disease; arteriosclerosis.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
DN	WO200063253-A1.		
XX	XX		
PD	26-OCT-2000.		
XX	XX		
PF	24-MAR-2000; 2000WO-US008004.		
XX	XX		
PR	16-APR-1999; 99US-00293245.		
XX	XX		
PA	(AMGE-) AMGEN INC.		
PI	Hsu H, Meng S;		
XX	XX		
DR	WPI; 2000-665240/64.		
DR	N-PSDB; AAC67831.		
XX	XX		
PT	Fusion protein of AGP-1 protein and an Fc region, used to treat		
PT	proliferative disorders, immune disorders, and virally-induced disorders.		
XX	XX		
PS	Claim 3; Fig 2; 93pp; English.		
XX	XX		
CC	The present sequence is human AGP-1, a type II transmembrane protein.		
CC	Fusion proteins comprising an Fc immunoglobulin region fused to the N-		
CC	terminal portion of the AGP-1 protein have been produced. The fusion		
CC	proteins can be used to induce apoptosis in a tissue, and to treat		
CC	proliferative disorders, immune disorders, or virally-induced disorders.		
CC	The proliferative disorders include cancers, such as breast, prostate,		
CC	lung or colon cancer. The viral infections include hepatitis, and		
CC	acquired immunodeficiency syndrome (AIDS), and the immune disorders may		
CC	be autoimmune disorders or transplant rejection. Cardiovascular disease		
CC	such as arteriosclerosis may also be treated. The AGP-1 containing fusion		
CC	proteins have increased biological activity compared to the soluble AGP-1		
CC	proteins used in prior art therapies		
XX	XX		



PA (GETH ) GENENTECH INC.  
 XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
 XX WPI; 2001-016509/02.  
 DR N-PSDB; AAC91579.  
 XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for  
 PT treating various tumors, e.g. breast cancer, and other inflammatory,  
 PT angiogenic and immunological disorders.  
 XX  
 PS Claim 31; Fig 54; 188pp; English.  
 XX  
 CC The present sequence is one of twenty eight novel PRO polypeptides. The  
 CC PRO polypeptides and their agonists, including antibodies, peptides, and  
 CC small molecule agonists, may be used to treat various tumours, e.g.,  
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
 CC central nervous system cancer, melanoma or leukaemia. They are also  
 CC useful for treating other disorders such as neuronal, glial, astrocytal,  
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and  
 CC blastocoeic disorders, and inflammatory, angiogenic and immunological  
 CC disorders  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 281; DB 4; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLKQMDKYSGIACFLKE 60  
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLKQMDKYSGIACFLKE 60  
 QY 61 DDSDYNDPNDDESMNSPCQVKQWLQRLVKMLRTSEETISTVQSKQNNISPLVRERGPO 120  
 Db 61 DDSDYNDPNDDESMNSPCQVKQWLQRLVKMLRTSEETISTVQSKQNNISPLVRERGPO 120  
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRQBEIKENTKNDKQVQIYKYTSYPPDILLMKSGARNCSWSDAEYGLY 240  
 Db 181 FYIYSQTYFRQBEIKENTKNDKQVQIYKYTSYPPDILLMKSGARNCSWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 RESULT 14  
 AAB67243  
 ID AAB67243 standard; protein; 281 AA.  
 AC AAB67243;  
 DT 18-APR-2001 (first entry)  
 XX Human Apo2 ligand.  
 DE Human; Apo2 ligand: divalent metal ions; viral infection; cancer.  
 KW Homo sapiens.  
 XX  
 OS WO200100832-A1.  
 XX  
 PN 04-JAN-2001.  
 XX  
 PD 26-JUN-2000; 2000WO-US017579.  
 XX  
 PF 28-JUN-1999; 99US-0141342P.  
 PR

XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;  
 PI O'connell M, Pai R, Shahrokh Z, Simmons L;  
 XX WPI; 2001-123012/13.  
 XX Use of divalent metal ions for making Apo-2 ligand and in formulations  
 PT containing Apo-2 ligand for increasing yield and stability of ligand  
 PT trimers, useful for therapeutic applications.  
 XX  
 PS Claim 6; Fig 1; 60pp; English.  
 XX  
 CC The present invention relates to a formulation comprising Apo-2 ligand  
 CC and divalent metal ions. Apo-2 ligand and the formulation are useful for  
 CC treating cancers and viral infections. Addition of divalent metal ions  
 CC for making Apo-2 ligand and formulations containing Apo-2 ligand results  
 CC in increased yield and stability of Apo-2 ligand trimers  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 281; DB 4; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLKQMDKYSGIACFLKE 60  
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLKQMDKYSGIACFLKE 60  
 QY 61 DDSDYNDPNDDESMNSPCQVKQWLQRLVKMLRTSEETISTVQSKQNNISPLVRERGPO 120  
 Db 61 DDSDYNDPNDDESMNSPCQVKQWLQRLVKMLRTSEETISTVQSKQNNISPLVRERGPO 120  
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
 QY 181 FYIYSQTYFRQBEIKENTKNDKQVQIYKYTSYPPDILLMKSGARNCSWSDAEYGLY 240  
 Db 181 FYIYSQTYFRQBEIKENTKNDKQVQIYKYTSYPPDILLMKSGARNCSWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 RESULT 15  
 AAE11031  
 ID AAE11031 standard; protein; 281 AA.  
 XX  
 AC AAE11031;  
 DT 18-DEC-2001 (first entry)  
 XX Human TNF related apoptosis inducing ligand (TRAIL) protein.  
 DE Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;  
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;  
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;  
 KW melanoma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Domain  
 FT /label= N-terminal\_cytoplasmic\_domain  
 FT 19..38  
 FT /label= Transmembrane\_region  
 FT 39..281  
 FT /label= Extracellular\_domain  
 XX  
 PN US284236-B1.

```
XX PD 04-SEP-2001.
XX PF
XX PF 26-MAY-1999; 99US-00320424.
XX PR
XX PR 29-JUN-1995; 95US-00496632.
XX PR 01-NOV-1995; 95US-00548368.
XX PR 25-JUN-1996; 96US-00670354.
XX PR 26-MAR-1998; 98US-00048641.
XX PR 10-NOV-1998; 98US-00190046.
XX PA (IMMV ) IMMUNEX CORP.
XX PI
XX PI Wiley SR, Goodwin RG;
XX DR
XX DR WPI; 2001-595463/67.
XX DR N-PSDB; AAD18395.
XX PT
XX PT New tumor necrosis factor related apoptosis inducing ligand polypeptides
XX PT for treating viral infections (e.g. bovine viral diarrhea or human
XX PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX PS
XX PS Claim 2; Col 45-48; 41pp; English.
XX CC
XX CC The invention relates to a cytokine designated as tumour necrosis factor
XX CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
XX CC of certain target cells, including cancer cells and virally infected
XX CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
XX CC treating viral infections (e.g. bovine viral diarrhoea or human
XX CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
XX CC melanoma), as a research reagent useful in studying apoptosis including
XX CC the regulation of programmed cell death. TRAIL DNA sequences may be
XX CC employed in developing a gene therapy approach to treating disorders
XX CC mediated by defective or insufficient amounts of TRAIL, in the production
XX CC of TRAIL polypeptides and as probes or primers in polymerase chain
XX CC reactions (PCR). The present sequence is human TRAIL protein
XX SQ
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNQLKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNQLKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 16
AAB48350
ID AAB48350 standard; protein; 281 AA.
XX
XX AAB48350;
XX AC
XX AC 20-APR-2001 (first entry)
XX DT
XX DE Human TL2 polypeptide.
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XX KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
XX KW anti-inflammatory; immunosuppressive; cerebroprotective; vasotropic;
XX KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;
XX KW neutropic; neuroprotective; antiarthritic; antirheumatic; antischismic;
XX KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
XX OS
XX OS Homo sapiens.
XX PN WO200077191-A1.
XX PD 21-DEC-2000.
XX PF
XX PF 12-JUN-2000; 2000WO-US016134.
XX PR
XX PR 15-JUN-1999; 99US-00333593.
XX PA (SMIK ) SMITHLINE BEECHAM CORP.
XX PI
XX PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
XX DR WPI; 2001-112223/12.
XX DR N-PSDB; AAC84745.
XX PT
XX PT New tumor necrosis factor related receptor TR6 polynucleotides and
XX PT polypeptides useful for e.g. for treating chronic and acute inflammation,
XX PT arthritis, septicemia, autoimmune diseases, infection, cancer, bone
XX PT diseases.
XX PS
XX PS Disclosure; Page 26; 47pp; English.
XX CC
XX CC The invention relates to a human tumour necrosis factor (TNF) related
XX CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.
XX CC The TR6 polypeptides are useful for treating chronic and acute
XX CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
XX CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
XX CC host disease, infection, stroke, ischaemia, acute respiratory disease
XX CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
XX CC atherosclerosis, and Alzheimer's disease. These may also be used to
XX CC inhibit production of TNF-alpha and eicosanoids, as research reagents and
XX CC materials for discovering treatments and diagnostics to animal and human
XX CC diseases. The polypeptides may further be used as immunogens to produce
XX CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides
XX CC may also be used as hybridization probes for cDNA and genomic DNA, for
XX CC isolating full-length cDNAs and genomic clones encoding TR6 and of other
XX CC genes having high sequence similarity to TR6 gene, and for chromosome
XX CC identification. The present sequence represents a human TL2 polypeptide.
XX CC TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is
XX CC a ligand for the TL2 polypeptide
XX SQ
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNQLKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNQLKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
|||||
RESULT 17
ABB08133
ID ABB08133 standard; protein; 281 AA.
XX
XX
AC ABB08133;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human TRAIL polypeptide.
DE
XX
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
KW tuberculostatic; cytostatic; human; TRAIL.
XX
XX Homo sapiens.
XX
XX WO200236141-A2.
XX
XX 10-MAY-2002..
XX
XX 30-OCT-2001; 2001WO-US044834.
XX
XX 02-NOV-2000; 2000US-024572LP.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
XX Thomas EK;
XX
XX WPI; 2002-500114/53.
XX
XX Treating an individual suffering from infection, e.g. inflammation,
XX chickenpox or AIDS, by administering a combination of dendritic cell
XX mobilization factor or maturation agent, T cell enhancing factor and
XX antigen-specific T cells.
XX
XX Disclosure; Page 40-42; 43pp; English.
XX
XX The invention relates to treating an individual at risk for or suffering
XX from infection with a pathogenic or opportunistic organism. The method
XX involves administering a combination of two to five agents comprising:
XX (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
XX agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
XX or (e) activated antigen-specific T cells. The methods are useful for
XX treating an individual at risk for or suffering from infection with a
XX pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
XX (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
XX T. cruzi, which causes Chaga's disease). The methods are especially
XX useful for treating an individual suffering from immunosuppression by
XX enhancing a lymphocyte-mediated immune response. In particular, the
XX method is useful for treating inflammations, chickenpox, oral or genital
XX herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
XX cell leukemia or T cell lymphoma. The activated antigen-presenting
XX dendritic cells are useful as a vaccine adjuvant. The present sequence
XX represents a human TRAIL polypeptide fragment
XX
XX Sequence 281 AA;
XX
Query Match      100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNKLQMDKYSGKIACFLKE 60
|||||
DB      1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNKLQMDKYSGKIACFLKE 60
|||||
QY      61 DDSYNDPNDDESNNSPCWQVKQLROLVRKMLRTSEETISTVQEKQNNISPLVRERGPO 120
|||||
DB      61 DDSYNDPNDDESNNSPCWQVKQLROLVRKMLRTSEETISTVQEKQNNISPLVRERGPO 120
|||||

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QY      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLHUNGELVTHEKG 180
|||||
DB      121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLHUNGELVTHEKG 180
|||||
QY      181 FYIYISQTYFRFOEIKENTKNDKQMVQYIYKYTSYPDPILLMKARNSCWSKDAEYGLY 240
|||||
DB      181 FYIYISQTYFRFOEIKENTKNDKQMVQYIYKYTSYPDPILLMKARNSCWSKDAEYGLY 240
|||||
QY      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
|||||
DB      241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
|||||

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RESULT 18
ABG31630
ID ABG31630 standard; protein; 281 AA.
XX
XX ABG31630;
XX
XX 29-NOV-2002 (first entry)
XX
XX Human TRAIL protein.
XX
XX Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
XX dendritic cell maturation agent; T cell enhancing factor; skin cancer;
XX antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
XX brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
XX actinic keratosis; dendritic cell maturation stimulator; cytostatic;
XX dendritic cell activator; T cell enhancer; human; TRAIL.
XX
XX Homo sapiens.
XX
XX WO200266044-A2.
XX
XX 29-AUG-2002.
XX
XX 23-OCT-2001; 2001WO-US046254.
XX
XX 24-OCT-2000; 2000US-0242868P.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;
XX WPI; 2002-674891/72.
XX
XX Treating an individual with tumors or cancers, e.g. liver cancer or brain
XX tumor, by administering a combination of dendritic cell populations, T
XX cell enhancing factors and activated, antigen-specific T cells.
XX
XX Disclosure; Page 41-43; 44pp; English.
XX
XX The present invention relates to a new method for treating a tumour-
XX bearing subject. The method involves administering a combination of 2 to
XX 5 agents comprising dendritic cell mobilisation factor, dendritic cell
XX maturation agent, tumour-killing agent, T cell enhancing factor or
XX activated, antigen-specific T cells. The method is useful for treating
XX tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
XX cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
XX cervical intraepithelial neoplasia. The present amino acid sequence
XX represents the human TRAIL protein that was used in the method of the
XX invention
XX
XX Sequence 281 AA;
XX
Query Match      100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNKLQMDKYSGKIACFLKE 60
|||||
DB      1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNKLQMDKYSGKIACFLKE 60
|||||

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QY 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120  
DB 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSF LSNLHRLNGELVIHKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSF LSNLHRLNGELVIHKG 180  
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYDPDPILLMKSARNCSKDAEYGLY 240  
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYDPDPILLMKSARNCSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 19  
AAU75062  
ID AAU75062 standard; protein; 281 AA.  
XX AAU75062;  
AC AAU75062;  
DT 23-APR-2002 (first entry)  
XX Human TNF related apoptosis inducing ligand (TRAIL) protein.  
DE TRAIL; TNF; apoptosis; tumour; death domain receptor ligand;  
KW diterpenoid triepoxide; cycostatic activity; C-IAP2; C-IAP1; carcinoma;  
KW mammary adenocarcinoma; non-small cell lung carcinoma;  
KW neurological malignancy; haematological malignancy; lichen planus;  
KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;  
KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;  
KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;  
KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;  
KW discoid lupus erythematosus; human.

XX Homo sapiens.  
XX US6329148-B1.  
XX 11-DEC-2001.  
XX 15-FEB-2000; 2000US-00505250.  
PR 16-FEB-1999; 99US-0120313P.  
PR 20-AUG-1999; 99US-0149989P.  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX Rosen GD, Kao P;  
PI WPI; 2002-121125/16.  
XX N-PSDB; ABK13192.  
XX Use of a synergistic combination of death domain receptor ligands and diterpenoid triepoxides for killing of tumor cells.  
XX Disclosure; Col 17-20; 20pp; English.

CC This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cycostatic activity and works by blocking TNF-alpha mediated induction of C-IAP2 and C-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered

CC with other active agents, e.g. anti- metastatic, anti-tumour or anti-angiogenic agents. The potent synergy between the diterpenoids and the death domain ligands allows increased killing at equivalent or lower doses, and can sensitize otherwise resistant cells. This sequence represents the human TNF related apoptosis inducing ligand (TRAIL) protein sequence. TRAIL is a death domain receptor used in the used method of the invention in combination with diterpenoid triepoxides to kill tumours by induction of apoptosis

XX Sequence 281 AA;  
Query Match 100.0%; Score 281; DB 5; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVTVVYFTNELKOMQDKYSKGIACFLKE 60  
DB 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCAVAVTVVYFTNELKOMQDKYSKGIACFLKE 60  
QY 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120  
DB 61 DDSYWDPNDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSF LSNLHRLNGELVIHKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSF LSNLHRLNGELVIHKG 180  
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYDPDPILLMKSARNCSKDAEYGLY 240  
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYDPDPILLMKSARNCSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 20  
AAM51077  
ID AAM51077 standard; protein; 281 AA.  
XX AAM51077;  
AC AAM51077;  
DT 30-MAY-2002 (first entry)  
XX Human Apo-2 ligand (TRAIL).  
DE Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour; antitumour; therapy.  
KW Homo sapiens.  
OS Key Location/Qualifiers  
FH Protein 114..281  
FT /note= "Apo-2L polypeptide used in method of Claim 18"  
XX WO200209755-A2.  
XX 07-FEB-2002.  
XX 27-JUL-2001; 2001WO-US023691.  
XX 27-JUL-2000; 2000US-0221256P.  
XX (GETH ) GENENTECH INC.  
XX Escandon E, Fox JA, Kelley SK, Xiang H;  
PI WPI; 2002-268997/31.  
XX Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I inhibitor class, and Apo-2 ligand receptor agonist for enhancing apoptosis in mammalian cells, or for treating cancer in a mammal.

PS Claim 19; Page 79-80; 84pp; English.

XX The present sequence is that of human Apo-2L ligand (Apo-2L or TRAIL). The

CC invention relates to methods of inducing apoptosis in mammalian cells,

CC and especially to the use of Apo-2L receptor agonists and CPT-11 (a

CC chemotherapeutic agent of the topoisomerase I inhibitor class) to

CC synergistically induce apoptosis in mammalian cells, in particular

CC mammalian cancer cells, and especially colorectal cancer cells (claimed).

CC The cells may be in cell culture or in a mammal, e.g. a mammal suffering

CC from cancer or a condition in which induction of apoptosis in the cells

CC is desirable. A claimed method of treating cancer in a mammal comprises

CC administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is

CC administered about 6-72 hours prior to administration of the Apo-2L

CC receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L

CC (especially amino acids 114-281 of the present sequence) and anti-DR4 or

CC anti-DR5 receptor antibodies. Exposure of the cancer cells to CPT-11 and

CC Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors,

CC directing the cells towards an apoptotic pathway rather than cell cycle

CC arrest and possible DNA repair, thus providing enhanced anticancer

CC activity. An example illustrates the synergistic inhibition of tumour

CC growth by Apo-2L and CPT-11 in athymic nude mice injected s.c. with human

CC COLO205 colon carcinoma cells

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.9e-266; Mismatches 0; Indels 0; Gaps 0;

Matches 281; Conservative 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSGARNCSKDAEYGLY 240

DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSGARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 21

ID ABP51954

XX ABP51954 standard; protein; 281 AA.

AC ABP51954;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human Apo-2 ligand protein sequence SEQ ID NO:4.

XX

KW Bacterial host; protease; degp; prc; spr; anti-VEGF antibody; antibody;

KW humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;

KW anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;

XX anti-CD11a; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab';

XX anti-VEGF Fab.

OS Homo sapiens.

XX

PN WO200248376-A2.

XX

PD 20-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-US047581.

XX

PR 14-DEC-2000; 2000US-0256162P.

PA (GETH ) GENENTECH INC.

PI Chen CY;

XX WPI; 2002-583522/62.

DR N-PSDB; ABQ73920.

XX

PT Novel Escherichia coli strain useful for producing polypeptide, deficient

PT in degp and prc encoding protease, and harboring mutant spr gene, product

PT of gene suppresses growth phenotypes of strains harboring prc mutants.

XX

PS Example 1; Fig 4; 63pp; English.

XX

CC The present invention describes an Escherichia coli strain (I) deficient

CC in chromosomal degp and prc encoding protease degp and prc, respectively,

CC and harbouring a mutant spr gene, the product of mutant spr gene

CC suppresses growth phenotypes exhibited by strains harbouring prc mutants.

CC (I) is useful for producing a polypeptide, by culturing (I) comprising

CC nucleic acid encoding the polypeptide, which is heterologous to the

CC strain, such that the nucleic acid is expressed, and recovering the

CC heterologous polypeptide from the strain. The heterologous polypeptide is

CC proteolytically sensitive. Culturing of (I) is performed in a fermentor

CC under conditions of high- or low-cell density fermentation. The

CC polypeptide is recovered from the periplasm or culture medium of the

CC strain. The polypeptide is an antibody (humanised or full-length

CC antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular

CC endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,

CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an

CC antibody fragment having a light chain (kappa light chain). The antibody

CC fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18

CC Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper

CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-

CC tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti

CC CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18

CC Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence

CC represents a human Apo-2 ligand amino acid sequence from the present

CC invention

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.9e-266; Mismatches 0; Indels 0; Gaps 0;

Matches 281; Conservative 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSGARNCSKDAEYGLY 240

DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYDPDPILLMKSGARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 22

ID AAO19095

XX AAO19095 standard; protein; 281 AA.

AC AAO19095;

XX

DT 22-NOV-2002 (first entry)  
XX C neoformans antigen expressing dendritic cell related protein #4.  
XX Human; fungicide; fungal infection; dendritic cell; antigen;  
KW Cryptococcus neoformans; vaccine; immunostimulant.  
XX Homo sapiens.  
XX WO200266053-A2.  
XX 29-AUG-2002.  
PD 14-DEC-2001; 2001WO-US048288.  
XX 04-JAN-2001; 2001US-0259653P.  
XX (IMMV ) IMMUNEX CORP.  
XX Thomas EK;  
XX WPI; 2002-674896/72.  
XX Producing a population of activated, Cryptococcus neoformans antigen-presenting dendritic cells for preventing or treating C. neoformans infection comprises causing the obtained dendritic cells to present the antigen.  
XX Disclosure; Page 29-30; 32pp; English.  
XX The present invention relates to a method of producing a population of activated, Cryptococcus neoformans antigen-presenting dendritic cells, comprising causing the obtained dendritic cells to present the antigen and maturing the dendritic cells. The activated, C. neoformans antigen-expressing dendritic cells are useful for treating, or as vaccines or vaccine adjuvants against, C. neoformans infection, or for generating antigen-specific T cells. The present sequence is a human protein shown in the exemplification of the invention  
XX Sequence 281 AA;  
SQ Query Match 100.0%; Score 281; DB 5; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSIGQTCVLIVIFVTLVLLQSI-CVAVTVYVFTNELKQMDKYSGIACFLKE 60  
DB 1 MAMMEVQGGPSIGQTCVLIVIFVTLVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQKQKNISPLVRERGQ 120  
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQKQKNISPLVRERGQ 120  
QY 121 RVAAHITGRSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHLRNGELVIHKG 180  
DB 121 RVAAHITGRSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHLRNGELVIHKG 180  
QY 181 FYIYISQYFRQBEIKENTKNDKQVQYIKYTSYPPDILLMKSRNSCKDAEYGLY 240  
DB 181 FYIYISQYFRQBEIKENTKNDKQVQYIKYTSYPPDILLMKSRNSCKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 281  
RESULT 23  
AAU79593  
ID AAU79593 standard; protein; 281 AA.  
XX AAU79593;  
AC AAU79593;  
XX 24-SEP-2002 (first entry)

XX Human TNF-related apoptosis inducing ligand (TRAIL) protein.  
XX Human; cytosolic; neuroprotective; immunosuppressive; splice variant;  
KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;  
KW TRAIL; apoptosis; programmed cell death; differentiation; development;  
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;  
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;  
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;  
KW chromosome 3q26.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Domain 1..16  
FT /note= "Cytoplasmic domain"  
FT Domain 17..38  
FT /note= "Transmembrane domain"  
FT Domain 39..281  
FT /note= "Extracellular domain"  
FT Domain 118..256  
FT /note= "TNF domain"  
XX US2002061525-A1.  
PW 23-MAY-2002.  
XX 16-MAY-2001; 2001US-00855544.  
XX 16-MAY-2000; 2000IL-00136156.  
XX (YELI/) YELIN R.  
PA (KHOS/) KHOSRAVI R.  
PA (SAVI/) SAVITZKY K.  
XX Yelin R, Khosravi R, Savitzky K;  
XX WPI; 2002-479259/51.  
XX New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.  
XX Disclosure; Fig 9; 29pp; English.  
XX The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumour necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms. Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1 and DcR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative

CC diseases, autoimmune diseases, diseases involved in the non-normal  
CC development of tissues and aging. TRAIL's gene is located on chromosome  
CC 3q26. The sequence presented is the wild-type human TNF-related apoptosis  
CC inducing ligand (TRAIL) protein  
XX  
XX  
SQ Sequence 281 AA;  
  
Query Match 100.0%; Score 281; DB 5; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAMVEQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60  
DB 1 MAMVEQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60  
  
QY 61 DSYWDPNDESMNSPCQVQKWLRLVKRMILRTSEETISTVQEKQKNISPLVRERGQ 120  
DB 61 DSYWDPNDESMNSPCQVQKWLRLVKRMILRTSEETISTVQEKQKNISPLVRERGQ 120  
  
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
  
QY 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKVTSPDPIILMKSGARNSCWSDAEYGLY 240  
DB 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKVTSPDPIILMKSGARNSCWSDAEYGLY 240  
  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
  
RESULT 24  
ABG73861  
ID ABG73861 standard; protein; 281 AA.  
XX  
AC ABG73861;  
XX  
DT 03-APR-2003 (first entry)  
XX  
DE Human Apo-2 ligand protein.  
XX  
KW Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;  
KW nuclear factor-kappa B; NF-kappa B; Apo-2 ligand; AIDS;  
KW tumour necrosis factor receptor; acquired immunodeficiency syndrome;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;  
KW aplastic anaemia; myocardial infarction; stroke; reperfusion injury;  
KW toxin-induced liver disease; cancer; lupus; herpes virus infection.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 15..40  
FT Domain /note= "Transmembrane domain"  
FT Domain 41..281  
FT Modified-site 109  
FT /note= "Extracellular domain"  
FT /note= "N-glycosylated"  
FN US462176-B1.  
XX  
PD 08-OCT-2002.  
XX  
PF 11-SEP-1997; 97US-00928069.  
XX  
PR 23-SEP-1996; 96US-0026943P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ;  
XX  
XX WPI; 2003-173840/17.

DR N-PSDB; ABX15469.  
XX  
PT Novel isolated Apo-3 polypeptide useful for inducing apoptosis in  
PT mammalian cells, for generating antibodies, in affinity purification  
PT techniques, and in competitive-type receptor binding assays.  
XX  
XX  
PS Example 4; Fig 4; 52pp; English.  
XX  
CC The invention relates to an Apo-3 polypeptide having an extracellular  
CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide  
CC has been found to stimulate or induce apoptotic activity in mammalian  
CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor  
CC receptor (TNFR) family of polypeptides. The invention also relates to a  
CC chimeric molecule comprising an extracellular domain sequence comprising  
CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The  
CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in  
CC mammalian cells. Decreased levels of apoptosis has been associated with  
CC conditions such as cancer, lupus, and herpes virus infection. Increased  
CC levels of apoptosis are associated with diseases such as acquired  
CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's  
CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis  
CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial  
CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.  
CC The Apo-3 polypeptide is also useful in non-therapeutic applications such  
CC as in quantitative diagnostic assays as a control against which samples  
CC containing unknown quantities of Apo-3 may be prepared, in generating  
CC antibodies, as standards in assays for Apo-3, in affinity purification  
CC techniques, and in competitive-type receptor binding assays. The chimeric  
CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor  
CC -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-  
CC Apo-3 antibodies. The present sequence represents polypeptide sequence of  
CC the human Apo-2 ligand protein which is also reported to be involved in  
CC apoptotic cell death. In the current invention the apoptotic activity of  
CC the Apo-2 ligand protein was measured on human lymphoid cells  
XX  
SQ Sequence 281 AA;  
  
Query Match 100.0%; Score 281; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAMVEQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60  
DB 1 MAMVEQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60  
  
QY 61 DSYWDPNDESMNSPCQVQKWLRLVKRMILRTSEETISTVQEKQKNISPLVRERGQ 120  
DB 61 DSYWDPNDESMNSPCQVQKWLRLVKRMILRTSEETISTVQEKQKNISPLVRERGQ 120  
  
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
  
QY 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKVTSPDPIILMKSGARNSCWSDAEYGLY 240  
DB 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKVTSPDPIILMKSGARNSCWSDAEYGLY 240  
  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
  
RESULT 25  
ABU10205  
ID ABU10205 standard; protein; 281 AA.  
XX  
AC ABU10205;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Human Apo-2 ligand.  
XX  
KW Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; cancer;



KW neurodegenerative disease; immunosuppressive; tissue typing.

OS Homo sapiens.

FN US2003004313-A1.

XX 02-JAN-2003.

XX 28-MAR-2002; 2002US-00112193.

XX 23-SEP-1996; 96US-0026943P.

PR 11-SEP-1997; 97US-00928069.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 2003-438872/41.

DR N-PSDB; ACA61696.

XX New isolated Apo-3 polypeptides, useful for stimulating or inducing  
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo  
PT or ex vivo gene therapy techniques.

XX Example 4; Fig 4; 50pp; English.

CC The invention relates to an isolated Apo-3 polypeptide. The Apo-3  
CC polypeptides are useful for stimulating or inducing apoptotic activity in  
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy  
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting  
CC apoptosis, or as immunogens used in generating antibodies. The  
CC antagonistic antibodies may be used to block excessive apoptosis, for  
CC instance in neurodegenerative disease, or to block potential autoimmune/  
CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The  
CC nucleic acid sequences are useful as diagnostics for tissue-specific  
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or  
CC knockout animals. The transgenic or knockout animals are useful in  
CC developing and screening of therapeutically useful reagents. The present  
CC sequence represents the amino acid sequence of human Apo-2 ligand

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.9e-266;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYVYTNELKQMDKYKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYVYTNELKQMDKYKSGIACFLKE 60

QY 61 DDSYWDPNDESMNSPCQVQWQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Db 61 DDSYWDPNDESMNSPCQVQWQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRQBEIKNTKNDKQMVQIYKYTSPDPILLMKSGARNSCSKDAEYGLY 240

Db 181 FYYIYSQTYFRQBEIKNTKNDKQMVQIYKYTSPDPILLMKSGARNSCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFVNG 281

Db 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFVNG 281

RESULT 26

ABU71443

ID ABU71443 standard; protein; 281 AA.

XX

AC ABU71443;

XX

DT 09-JUN-2003 (first entry)

XX Human neoplasia inhibiting PRO polypeptide PRO1096.

XX Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;  
KW ovarian cancer; renal cancer; colorectal cancer; melanoma;  
KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;  
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;  
KW central nervous system cancer; hepatic carcinoma; glioblastoma;  
KW neuronal disorder; glial disorder; astrocytal disorder;  
KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
KW epithelial disorder; stromal disorder; blastocoelec disorder;  
KW inflammatory disorder; angiogenic disorder; immunologic disorder.

XX Homo sapiens.

FN US2002192209-A1.

XX 19-DEC-2002.

XX 30-NOV-2001; 2001US-00001054.

PR 17-SEP-1997; 97US-0059114P.

PR 27-MAR-1998; 98US-0079689P.

PR 30-MAR-1998; 98US-0079920P.

PR 24-APR-1998; 98US-0082999P.

PR 29-APR-1998; 98US-0083545P.

PR 12-MAY-1998; 98US-0085149P.

PR 02-JUN-1998; 98US-0087607P.

PR 11-JUN-1998; 98US-0088858P.

PR 25-JUN-1998; 98US-0090691P.

PR 17-AUG-1998; 98US-0096891P.

PR 17-AUG-1998; 98US-0096894P.

PR 10-SEP-1998; 98US-0099803P.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98US-0100263P.

PR 15-SEP-1998; 98US-0100390P.

PR 23-SEP-1998; 98US-0101476P.

PR 10-NOV-1998; 98US-0107783P.

PR 18-NOV-1998; 98US-010849P.

PR 19-NOV-1998; 98US-00180997.

PR 15-DEC-1998; 98US-0112420P.

PR 22-DEC-1998; 98US-00218517.

PR 22-DEC-1998; 98US-0113296P.

PR 05-JAN-1999; 99WO-US000106.

PR 12-JAN-1999; 99US-0115554P.

PR 12-JAN-1999; 99US-0115558P.

PR 20-JAN-1999; 99US-0116533P.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99US-0123618P.

PR 12-APR-1999; 99US-00284291.

PR 20-APR-1999; 99WO-US008615.

PR 27-APR-1999; 99US-0131294P.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-014037P.

PR 20-JUL-1999; 99US-0144758P.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 09-SEP-1999; 99US-00380913.

PR 18-OCT-1999; 99US-00403297.

PR 29-OCT-1999; 99US-0162506P.

PR 10-NOV-1999; 99US-00423741.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028634.

PR 09-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99US-0170262P.

PR 20-DEC-1999; 99WO-US030095.

PR 06-JAN-2000; 99WO-US030999.

PR 11-FEB-2000; 2000WO-US000376.

PR 2000WO-US0003565.







FT FT /note= "N-terminal fragment specifically claimed in claim  
FT 124. .276  
FT /note= "This region is specifically claimed in claim 20"  
FT 276. .281  
FT /note= "C-terminal fragment specifically claimed in claim  
FT 26"  
XX  
PN US6521228-B1.  
XX  
PD 18-FEB-2003.  
XX  
PP 02-APR-2001; 2001US-00825563.  
XX  
PR 29-JUN-1995; 95US-00496632.  
PR 01-NOV-1995; 95US-00548368.  
PR 26-JUN-1996; 96US-00670354.  
PR 26-MAR-1998; 98US-00048641.  
PR 10-NOV-1998; 98US-00190046.  
PR 26-MAY-1999; 99US-00320424.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Wiley SR, Goodwin RG;  
XX  
XX WPI; 2003-340628/32.  
DR N-PSDB; ABX93869.  
DR  
XX  
XX Novel antibody which binds to human tumor necrosis factor related  
PT apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated  
PT apoptosis of a target cell, or blocking binding of TRAIL to a target  
PT cell.  
XX  
PS Claim 1; Col 45-48; 40pp; English.  
XX  
XX The invention relates to an antibody that specifically binds: (a) the  
CC human tumor necrosis factor (TNF) related apoptosis inducing ligand  
CC (TRAIL) protein appearing as AB008558; (b) a soluble human TRAIL  
CC polypeptide; (c) a polypeptide comprising amino acids 124-276 of  
CC AB008558, or (d) a fragment of the TRAIL protein. Also included is an  
CC antigen-binding fragment of the antibody (a monoclonal antibody), a  
CC hybridoma cell line that produces the antibody. The antibody is used in  
CC assays to detect the presence of TRAIL polypeptides, either in vitro or  
CC in vivo, purifying TRAIL by affinity chromatography, blocking binding of  
CC TRAIL to target cells and thus inhibiting a biological activity of TRAIL.  
CC The antibody is useful for treating disorders mediated or exacerbated by  
CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic  
CC thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)  
CC (even though it can strike children as well), small blood vessel clotting  
CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic  
CC lupus erythematosus (SLE). The present sequence represents human TRAIL  
XX  
SQ Sequence 281 AA;  
Query Match 100.0%; Score 281; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYSGIACFLKE 60  
QY 61 DDSYNDPNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120  
DB 61 DDSYNDPNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIHEKG 180  
QY 181 FYIYISQTYFRQEETIKENTKNDKQWQVIYKYTSPDPDILLMKARNSCWSKDAEYGLY 240  
DB 181 FYIYISQTYFRQEETIKENTKNDKQWQVIYKYTSPDPDILLMKARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
RESULT 30  
ABR42313  
ID ABR42313 standard; protein; 281 AA.  
XX  
AC ABR42313;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Human TRAIL protein.  
XX  
KW Human; TRAIL; tumour necrosis factor; ligand; cytostatic;  
KW immunomodulator; osteopathic.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040307-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 25-JUL-2002; 2002WO-US023782.  
XX  
PR 27-JUL-2001; 2001US-0307838P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Hilbert DH, Rosen CA;  
XX  
DR WPI; 2003-430659/40.  
DR N-PSDB; ACC57899.  
XX  
XX New heteromultimeric complex having a first polypeptide member of the  
PT tumor necrosis factor (TNF) ligand family, and a second different member  
PT of TNF ligand family, useful for treating cancer, osteoporosis or an  
PT autoimmune disease.  
XX  
PS Disclosure; Page 364-365; 388pp; English.  
XX  
XX The present sequence is the protein sequence of human TRAIL polypeptide.  
CC The invention relates to compositions comprising heterotrimeric complexes  
CC of tumour necrosis factor (TNF) ligand family members, and their use in  
CC the detection, prevention and treatment of disease. In one embodiment,  
CC the heterotrimeric complex comprises full-length or extracellular  
CC portions of TRAIL and full-length or extracellular portions of other TNF  
CC ligand family members, preferably RANKL. The heterotrimeric complexes of  
CC the invention are useful for treating an autoimmune disease, cancer or  
CC osteoporosis, and particularly for inhibiting cancer cell proliferation,  
CC increasing B cell proliferation, or inducing apoptosis of T cells. A  
CC claimed method of inducing apoptosis of T cells comprises administering a  
CC heterotrimeric complex consisting of FasL and LIGHT, TNF-alpha,  
CC lymphotxin-beta or TRAIL. A claimed method of inhibiting cancer cell  
CC proliferation involves administering a heterotrimeric complex consisting  
CC of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis  
CC comprises administering an antibody against a complex comprising RANKL  
CC and TRAIL  
XX  
SQ Sequence 281 AA;  
Query Match 100.0%; Score 281; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVVYFTNELKQMDKYSGIACFLKE 60  
QY 61 DDSYNDPNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120

Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQKQNI9PLVRERGQ 120  
 Qy 121 RVAAHITGRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
 Db 121 RVAAHITGRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
 Qy 181 FYIYISQTYFRFQBEIKENTKNDKQVQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240  
 Db 181 FYIYISQTYFRFQBEIKENTKNDKQVQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240  
 Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 31

ID ABG71905 standard; protein; 281 AA.

AC ABG71905;

DT 20-JAN-2003 (first entry)

XX Human TRAIL receptor-associated protein.

XX Human; TRAIL receptor; tumour necrosis factor; TNF;  
 KW light chain variable region TNF-related apoptosis-inducing ligand;  
 KW antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7;  
 KW TR10; apoptosis; hyperproliferative disorder; hybridoma cell line;  
 KW Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease;  
 KW AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; autoimmune disorder;  
 KW multiple sclerosis; Behcet's disease; lupus erythematosus;  
 KW inflammatory disease; rheumatoid arthritis; psoriasis; wound healing;  
 KW cardiovascular disorder; angiogenesis; immune response;  
 KW chemotherapeutic agent.

XX Homo sapiens.

XX WO200279377-A2.

XX 10-OCT-2002.

XX 07-NOV-2001; 2001WO-US042996.

XX 08-NOV-2000; 2000US-0246612P.

XX 16-NOV-2000; 2000US-0248847P.

XX 27-NOV-2000; 2000US-0252904P.

XX 04-JUN-2001; 2001US-0295018P.

XX 09-OCT-2001; 2001US-0327359P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Salcedo T, Roschke V, Ruben SM, Rosen CA;

XX WPI; 2003-040669/03.

XX Novel antibody for treating, or preventing disease or disorder, comprises

XX amino acid sequence having identity to other amino acid sequence of

XX either variable heavy/light chain-complementarity determining regions.

XX Disclosure; Page 366; 375pp; English.

XX The invention relates to an isolated antibody comprising a first amino  
 CC acid sequence having 95 % identity to a second amino acid sequence of  
 CC either variable heavy chain or light chain-complementarity determining  
 CC regions (VHCDR1)/VHCDR2/VHCDR3 or VHCDR3/VHCDR3 appearing as  
 CC ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF  
 CC (tumour necrosis factor)-related apoptosis-inducing ligand receptor, also  
 CC known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that  
 CC produces the antibody, an antibody that binds the same epitope on a TR4  
 CC polypeptide as the antibodies detailed above, detecting expression of a  
 CC TR4 polypeptide( or detecting, diagnosing, prognosis or monitoring

CC cancers, and other hyperproliferative disorders) using the antibodies, a  
 CC hybridoma cell line selected from the hybridoma cell lines contained in  
 CC ATCC Deposit No. PTA-3149, PTA-2687, PTA-3369, PTA-2730, PTA-2729, PTA-  
 CC 2728, PTA-3369, and PTA-2731 and the antibodies expressed by these  
 CC hybridoma cell lines. The antibodies of the invention are useful for  
 CC diagnosing or treating a disease or disorder associated with increased or  
 CC decreased apoptosis, e.g. cancer (such as colon, breast, uterine,  
 CC pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versus-  
 CC host disease (GVHD), infectious disease, acquired immunodeficiency  
 CC syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Parkinson's disease), autoimmune disorders like multiple  
 CC sclerosis, Behcet's disease, lupus erythematosus, inflammatory diseases  
 CC such as rheumatoid arthritis, and psoriasis, cardiovascular disorders, in  
 CC promoting angiogenesis, wound healing, and in regulating immune response.  
 CC Many other diseases and disorders are listed in the specification. The  
 CC antibody is administered in combination with a chemotherapeutic agent  
 CC selected from irinotecan, paclitaxel (TAXOL (RPM)), and gemcitabine. The  
 CC antibody is useful as a diagnostic tool to monitor the expression of  
 CC TRAIL receptor expression on cells, to detect, purify, and target the  
 CC polypeptides, and in immunoassays for qualitatively and quantitatively  
 CC measuring levels of TRAIL receptor polypeptides. The present sequence is  
 CC a human TRAIL receptor associated protein. Note: The present sequence is  
 CC included in the sequence listing but is not referred to anywhere else in  
 CC the specification

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.9e-266;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVFTNELKQMDKYKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQKQNI9PLVRERGQ 120

Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQKQNI9PLVRERGQ 120

Qy 121 RVAAHITGRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

Db 121 RVAAHITGRGSRNTLSSPNSKNEALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

Qy 181 FYIYISQTYFRFQBEIKENTKNDKQVQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240

Db 181 FYIYISQTYFRFQBEIKENTKNDKQVQYIYKTSYTPDPILLMKSARNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 32

ABP60546

ID ABP60546 standard; protein; 281 AA.

XX AC ABP60546;

XX 28-MAR-2003 (first entry)

XX Human tumour necrosis factor TRAIL.

XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;  
 KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;  
 KW antiarthritic; cytostatic; antianaemic; antiallergic; antidiabetic;  
 KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;  
 KW antiposrotic; anti-Hiv; antiarteriosclerotic; vasotrophic; thyromimetic;  
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;  
 KW inflammatory disorder; proliferative disorder; single chain antibody;  
 KW antibody; human; TRAIL; tumour necrosis factor.

XX Homo sapiens.

XX OS

PN WO200294192-A2.  
 XX 28-NOV-2002.  
 PD  
 XX  
 PF 22-MAY-2002; 2002WO-US016106.  
 XX  
 PR 24-MAY-2001; 2001US-0293100P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Ruben SM;  
 XX WPI; 2003-156740/15.  
 DR  
 XX Novel isolated antibody that immunospecifically binds tumor necrosis  
 PT factor delta, useful for treating, preventing or ameliorating Non-  
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's  
 PT syndrome.  
 XX  
 PS Disclosure; Page 216-217; 225pp; English.  
 CC The invention relates to a novel antibody or its fragment, which  
 CC immunospecifically binds tumor necrosis factor Delta (TNF-delta/APRIL).  
 CC The antibody of the invention has dermatological, immunosuppressive,  
 CC antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,  
 CC antiallergic, antiasthmatic, neuroprotective, ophthalmological,  
 CC tuberculosic, antidiabetic, antipsoriatic, anti-HIV,  
 CC antiarteriosclerotic, vasotropic, thymimetic, and haemostatic activity.  
 CC The antibody or its fragment are useful for treating, preventing or  
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in  
 CC human, disease or disorder such as autoimmune disease, and graft versus  
 CC host disease (GVHD). The autoimmune disease is systemic lupus  
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody  
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or  
 CC ameliorating a disease or disorder associated with aberrant APRIL or  
 CC APRIL receptor expression or aberrant function of APRIL or APRIL  
 CC receptor. The disease or disorders includes autoimmune and inflammatory  
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,  
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,  
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune  
 CC system, particularly B cell cancers, immune disorders such as myasthenia  
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,  
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and  
 CC proliferative disorders (e.g. leukemia). The present sequence represents  
 CC the tumour necrosis factor TRAIL  
 XX  
 SQ Sequence 281 AA;  
 Query Match 100.0%; Score 281; DB 6; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVITFVLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVITFVLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60  
 QY 61 DSDYNDPNDDESNPCWQVKQLRQVVKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 DB 61 DSDYNDPNDDESNPCWQVKQLRQVVKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 QY 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHFLNLHRLNGELVIHEKG 180  
 DB 121 RVAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHFLNLHRLNGELVIHEKG 180  
 QY 181 FYYIVSOTYFRQEEIKENTKDKQWQVIYKYTSYDPDPFILMKNSARNCSWKDAEYGLY 240  
 DB 181 FYYIVSOTYFRQEEIKENTKDKQWQVIYKYTSYDPDPFILMKNSARNCSWKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 33  
 AAE36258  
 ID AAE36258 standard; protein; 281 AA.  
 XX  
 AC AAE36258;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human TR4 ligand, TRAIL protein.  
 XX  
 KW TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration;  
 KW hyperproliferative disorder; neurodegenerative disorder; immune disorder;  
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
 KW retinitis pigmentosa; Huntington's disease; Hashimoto's thyroiditis;  
 KW rheumatoid arthritis; multiple sclerosis; Sjogren's syndrome; asthma;  
 KW biliary cirrhosis; Behcet's disease; Crohn's disease; allergic disorder;  
 KW glomerulonephritis; immune deficiency syndrome; myasthenia gravis;  
 KW polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock;  
 KW infectious disease; acquired immunodeficiency syndrome; viral infection;  
 KW AIDS; proliferative disorder; myocardial infarction; reperfusion injury; cachexia;  
 KW ischaemic injury; myocardial infarction; reperfusion injury; cachexia;  
 KW anorexia; stroke; cardiovascular disorder; peripheral artery disease;  
 KW limb ischaemia; arrhythmia; congestive heart failure; neovascularisation;  
 KW ocular disorder; wound healing; angiogenesis; transplantation; human.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200297033-A2.  
 XX  
 05-DEC-2002.  
 XX  
 07-MAY-2002; 2002WO-US014268.  
 XX  
 25-MAY-2001; 2001US-0293473P.  
 PR 04-JUN-2001; 2001US-0294981P.  
 PR 02-AUG-2001; 2001US-0309176P.  
 PR 21-SEP-2001; 2001US-0323807P.  
 PR 09-OCT-2001; 2001US-0327364P.  
 PR 07-NOV-2001; 2001US-0331044P.  
 PR 14-NOV-2001; 2001US-0331310P.  
 PR 20-DEC-2001; 2001US-0341237P.  
 PR 05-APR-2002; 2002US-0369860P.  
 XX  
 (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Salcedo T, Ruben SM, Rosen CA, Albert VR, Dobson CL, Vaughan TJ;  
 PI  
 WPI; 2003-140454/13.  
 DR  
 XX Novel antibody useful for treating cancers and other hyperproliferative  
 PT disorders, immunospecifically binds to TRAIL receptor and comprises  
 PT variable heavy or light chain complementarity determining regions.  
 XX  
 PS Disclosure; Page 300-301; 301pp; English.  
 CC The present invention relates to novel antibodies that immunospecifically  
 CC bind to TRAIL receptor (TR4). Sequences of the invention are useful for  
 CC treating, preventing or ameliorating cancer (e.g. colon, breast, uterine,  
 CC pancreatic, lung, gastrointestinal or central nervous system cancer e.g.  
 CC medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in  
 CC human. They are useful for detecting expression of TR4 polypeptide and  
 CC detecting, diagnosing, prognosing or monitoring cancers and other hyper-  
 CC proliferative disorders. Antibodies of the invention are useful for  
 CC treating, preventing or ameliorating neurodegenerative disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
 CC retinitis pigmentosa, cerebellar degeneration and Huntington's disease),  
 CC immune disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis,  
 CC Sjogren's syndrome, biliary cirrhosis, Behcet's disease, Crohn's disease,  
 CC polymyositis, immune-related glomerulonephritis, myasthenia gravis,  
 CC Hashimoto's thyroiditis and immune deficiency syndrome), inflammatory  
 CC disorders (e.g. asthma, allergic disorders and rheumatoid arthritis),  
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)),  
 CC herpes viral infections and other viral infections) and proliferative

disorders. They are also useful for treating myelodysplastic syndromes (e.g. aplastic anaemia), ischaemic injury (such as that caused by stroke, myocardial infarction and reperfusion injury), septic shock, cachexia, anorexia and toxin-induced liver diseases (such as alcohol). They are also useful for treating cardiovascular disorders including peripheral artery diseases such as limb ischaemia, arrhythmia, congestive heart failure and cardiovascular tuberculosis, diseases or disorders associated with neovascularisation and ocular disorders, for wound healing, for promoting angiogenesis and as adjuvants to enhance immune responsiveness to specific antigen e.g. viral antigen. They are also useful in the preparation or recovery from surgery, trauma, radiation therapy and transplantation. The present sequence is human TR4 ligand, TRAIL protein used in the invention

XX  
SQ

Query Match 100.0%; Score 281; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 34  
AAO31151  
ID AAO31151 standard; protein; 281 AA.  
AC AAO31151;  
XX  
XX  
DT 06-OCT-2003 (first entry)  
XX  
DE Human TNF-related apoptosis-inducing ligand (TRAIL).  
XX  
KW Human; protein coordinate data; heavy chain variable domain; VH; cancer;  
KW complementarity determining region; CDR; light chain variable domain; VL;  
KW TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;  
KW DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;  
KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;  
KW glioblastoma; graft versus host disease; antibody therapy; neotropic;  
KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;  
KW immunosuppressive; neuroprotective; antibody therapy; antibody.  
XX  
OS Homo sapiens.  
XX  
XX WO2003054216-A2.  
XX  
PD 03-JUL-2003.  
XX  
PF 19-DEC-2002; 2002WO-US040597.  
XX  
XX 20-DEC-2001; 2001US-0341237P.  
PR 05-APR-2002; 2002US-0369877P.  
PR 04-JUN-2002; 2002US-0384828P.  
PR 18-JUL-2002; 2002US-0396591P.  
PR 15-AUG-2002; 2002US-0403370P.

PR 13-NOV-2002; 2002US-0425737P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;  
XX  
XX WPI; 2003-569250/53.  
DR  
XX  
XX New antibody or its fragment, useful for treating, preventing or  
PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or  
PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host  
PT disease, AIDS.  
XX  
XX  
PS Disclosure; Page 297-298; 301pp; English.  
XX  
XX The invention relates to an isolated antibody or its fragments such as  
CC VHCDR1 (heavy chain variable domain complementarity determining region),  
CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity  
CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment  
CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related  
CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as  
CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The  
CC antibody or its fragment is useful for treating, preventing or  
CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or  
CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central  
CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or  
CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or  
CC a neurodegenerative disorder. The invention is useful in antibody  
CC therapy. The present sequence is human TRAIL  
XX  
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60

Qy 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

Qy 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDILLMKSRNSCWSKDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 35  
ABO25125  
ID ABO25125 standard; protein; 281 AA.  
XX  
XX ABO25125;  
XX  
XX  
DT 05-SEP-2003 (first entry)  
XX  
DE Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.  
XX  
KW Human; DNA methylation; cancer; colon cancer.  
XX  
OS Homo sapiens.  
XX  
XX US2003013099-A1.  
PN  
XX





Db 181 FYIYISQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 37  
 ADC35202  
 ID ADC35202 standard; protein; 281 AA.  
 XX  
 AC ADC35202;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human TNF ligand family member #10.  
 XX  
 KW human; tumour necrosis factor; TNF ligand; endokine alpha;  
 KW excessive bone resorption disorder; osteoporosis; Paget's disease;  
 KW arterial calcification.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003100074-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 PF 15-AUG-2002; 2002US-00218547.  
 XX  
 PR 16-AUG-2001; 2001US-0312542P.  
 PR 30-OCT-2001; 2001US-0330761P.  
 XX  
 PA (YUGG/) YU G.  
 PA (NIJJ/) NI J.  
 PA (ROSE/) ROSEN C A.  
 PA (NARD/) NARDELLI B.  
 XX  
 PI Yu G, Ni J, Rosen CA, Nardelli B;  
 XX  
 DR WPI; 2003-696072/66.  
 DR N-PSDB; ADC35201.  
 XX  
 PT New Endokine alpha gene useful for preparing a composition for treating a  
 PT disease associated with excessive or insufficient bone resorption e.g.,  
 PT osteoporosis, Paget's disease or arterial calcification.  
 XX  
 PS Disclosure; SEQ ID NO 20; 145pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule encoding a  
 CC tumour necrosis factor family ligand. A composition comprising the  
 CC isolated antibody or its fragment is used for treating an individual in  
 CC need of decreased level of endokine alpha activity. The endokine alpha  
 CC polypeptide present in a heterotrimeric complex is used for treating an  
 CC individual having a disorder associated with excessive bone resorption,  
 CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an  
 CC individual having a disorder associated with insufficient bone resorption  
 CC comprises administering an endokine alpha antagonist, which is the  
 CC antibody that binds specifically to endokine alpha polypeptide. The  
 CC present sequence represents the amino acid sequence of a tumour necrosis  
 CC factor family ligand.  
 XX  
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60  
 Db 1 MAMMEVQGGPSLGQTCVLIVFTLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60  
 QY 61 DDSYWDPNDESMNSPCQVQKWLQRLVTKMLRTSEETISTVQSKQONISPLVREGRQ 120

Db 61 DDSYWDPNDESMNSPCQVQKWLQRLVTKMLRTSEETISTVQSKQONISPLVREGRQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLRLRGELVIHEKG 180  
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLRLRGELVIHEKG 180  
 QY 181 FYIYISQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240  
 Db 181 FYIYISQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 38  
 ADD14080  
 ID ADD14080 standard; protein; 281 AA.  
 XX  
 AC ADD14080;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human src biomarker polypeptide SEQ ID NO:269.  
 XX  
 KW predictor set; protein tyrosine kinase activity modulator;  
 KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;  
 KW gene therapy; drug sensitivity; genetic profile; cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003062395-A2.  
 XX  
 PD 31-JUL-2003.  
 XX  
 PF 17-JAN-2003; 2003WO-US001981.  
 PR 18-JAN-2002; 2002US-0350061P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Huang P, Fairchild CR, Lee FY, Shaw P;  
 XX  
 DR WPI; 2003-636735/60.  
 DR N-PSDB; ADD14676.  
 XX  
 PT New polynucleotides and polypeptides for predicting the activity of  
 PT compounds that interact with protein tyrosine kinases and/or protein  
 PT tyrosine kinase pathways.  
 XX  
 PS Claim 10; SEQ ID NO 269; 139pp; English.  
 XX  
 CC The present invention describes a predictor set comprising a plurality of  
 CC polynucleotides or polypeptides whose expression pattern is predictive of  
 CC the response of cells to treatment with a compound that modulates protein  
 CC tyrosine kinase activity or members of the protein tyrosine kinase  
 CC pathway. Also described: (1) predicting whether a compound is capable of  
 CC modulating the activity of cells, comprising obtaining a sample of cells,  
 CC determining whether the cells express a plurality of markers, and  
 CC correlating the expression of the markers to the compound's ability to  
 CC modulate the activity of the cells; (2) a plurality of cell lines for  
 CC identifying polynucleotides and polypeptides whose expression levels  
 CC correlate with compound sensitivity or resistance of cells associated  
 CC with a disease state; and (3) identifying polynucleotides and  
 CC polypeptides that predict compound sensitivity or resistance of cells  
 CC associated with a disease state, comprising subjecting the plurality of  
 CC cell lines to one or more compounds, analysing the expression pattern of  
 CC a microarray of polynucleotides or polypeptides, and selecting  
 CC polynucleotides or polypeptides that predict the sensitivity or  
 CC resistance of cells associated with a disease state by using the  
 CC expression pattern of the microarray. The polynucleotides and  
 CC polypeptides have cytostatic activities, and can be used in gene therapy.  
 CC The polynucleotides and polypeptides are useful in predicting the



CC activity of compounds that interact with protein tyrosine kinases and/or  
 CC protein tyrosine kinase pathways. These may be used in determining drug  
 CC sensitivity in patients to allow the development of individualized  
 CC genetic profiles which aid in treating diseases and disorders (e.g.  
 CC cancer) based on patient response at a molecular level. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNISPVLVRERGQ 120  
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNISPVLVRERGQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSGARNSCWSDAEYGLY 240  
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSGARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 39  
 ADD19010  
 ID ADD19010 standard; protein; 281 AA.  
 AC ADD19010;  
 DT 15-JAN-2004 (first entry)  
 XX Human disease related protein SeqID499.  
 XX human; disease state; cystostatic; antiinflammatory; ophthalmological;  
 KW antiarteriosclerotic; vulnary; gene therapy;  
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;  
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;  
 KW glucose transportation; catecholamine synthesis; iron transport;  
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;  
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;  
 KW inflammatory condition; wound healing.  
 XX Homo sapiens.  
 XX WO2003018621-A2.  
 PN 06-MAR-2003.  
 XX 23-AUG-2002; 2002WO-GB003892.  
 PF 23-AUG-2001; 2001GB-00020558.  
 PR 05-OCT-2001; 2001GB-00024037.  
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
 PA Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;  
 XX WPI; 2003-290046/28.  
 DR N-PSDB; ADD19011.  
 XX New substantially purified polypeptide, useful for diagnosing or treating  
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion

PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or  
 PT wound healing.  
 XX Claim 25; SEQ ID NO 499; 424pp; English.  
 XX This invention relates to novel human genes and gene product which are  
 CC implicated in certain disease states. Compounds which modulate the  
 CC proteins of the invention may have cystostatic, antiinflammatory, the  
 CC ophthalmological, antiarteriosclerotic or vulnary activities. The  
 CC sequences of the invention may be useful for gene therapy. The invention  
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,  
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,  
 CC erythropoiesis, or the biological response to hypoxia conditions  
 CC including processes such as glycolysis, gluconeogenesis, glucose  
 CC transportation, catecholamine synthesis, iron transport or nitric oxide  
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion  
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,  
 CC inflammatory conditions or wound healing. The present sequence is that of  
 CC a disease related protein of the invention.  
 XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNISPVLVRERGQ 120  
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQVLRKMLRTSEETISTVQEQQNISPVLVRERGQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
 QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSGARNSCWSDAEYGLY 240  
 DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKTSYTPDPILLMKSGARNSCWSDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 40  
 ABW02276

ID ABW02276 standard; protein; 281 AA.

AC ABW02276;

DT 12-FEB-2004 (first entry)

DE Human TRAIL protein.

KW Gastrointestinal tract disorder; tumour necrosis factor; TNF; DR3; TR6;  
 KW TNF-gamma-beta protein; inflammatory bowel disease; Crohn's disease;  
 KW ulcerative colitis; TRAIL; human.

OS Homo sapiens.

XX US2003198640-A1.

XX 23-OCT-2003.

XX 06-DEC-2002; 2002US-00310793.

XX 07-NOV-1994; 94WO-US012880.

PR 05-JUN-1995; 95US-00461246.

PR 09-JAN-1998; 98US-00005020.

PR 09-FEB-1998; 98US-0074047P.



Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 42

ADK72311

ID ADK72311 standard; protein; 281 AA.

XX ADK72311;

AC ADK72311;

XX 06-MAY-2004 (first entry)

XX Human Apo-2 ligand with potential substitutions highlighted #4.

DE Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;

KW variant; cancer; immune system disease; arthritis; multiple sclerosis;

KW human.

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers

FT Misc-difference 189

FT /note= "wild-type Tyr may be substituted by Ala, Ser or

FT Xaa (where Xaa is encoded by an amber codon) at this

FT location in the variant referred to in claim 17"

FT Misc-difference 191

FT /note= "wild-type Arg may be substituted by Lys at this

FT location in the variant referred to in claim 17"

FT Misc-difference 193

FT /note= "wild-type Gln may be substituted by Arg at this

FT location in the variant referred to in claim 17"

FT Misc-difference 264

FT /note= "wild-type His may be substituted by Arg, Asp,

FT Asn, Ala, Pro or Thr at this location in the variant

FT referred to in claim 17"

FT Misc-difference 266

FT /note= "wild-type Ile may be substituted by Val or Leu at

FT this location in the variant referred to in claim 17"

FT Misc-difference 267

FT /note= "wild-type Asp may be substituted by Asn, Glu or

FT Gln at this location in the variant referred to in claim

FT 17"

XX

PN WO2004001009-A2.

XX

XX 31-DEC-2003.

XX

XX 23-JUN-2003; 2003WO-US019750.

XX

XX 24-JUN-2002; 2002US-0391050P.

XX (GETH ) GENENTECH INC.

XX Hymowitz S, Kelley RF, Lindstrom SH;

PI WPI; 2004-082490/08.

DR

XX New Apo-2 ligand variant polypeptide, useful for preparing a composition

PT for treating cancer or immune-related disease, e.g., arthritis or

PT multiple sclerosis.

XX

PS Claim 17; SEQ ID NO 1; 111pp; English.

XX

CC The invention relates to a novel isolated Apo-2 ligand variant

CC polypeptide, comprising a sequence that differs from the native sequence

CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having

CC one or more following amino acid substitutions at the residue positions

CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an

CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand

CC variant polypeptide. Further disclosed are a composition comprising the

CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a

CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant

CC polypeptide is useful for preparing a composition for treating cancer or

CC immune-related disease, e.g., arthritis or multiple sclerosis. The

CC current sequence represents the human Apo-2 ligand amino acid sequence.

CC Note: The variant sequence that is referred to in claim 17 may contain

CC one or more of the potential substitutions highlighted in the features

CC table for this record.

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.9e-266; Indels 0; Gaps 0;

Matches 281; Conservative 0; Mismatches 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGKIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNELKQMDKYSGKIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQVLVKMLRTSEETISTVQSKQKNISPLVRERGQ 120

DB 61 DDSYWDPNDEESMNSPCQVKWQLRQVLVKMLRTSEETISTVQSKQKNISPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180

QY 181 FYIYSQTYERFQBEIKENTKNDKQMVQYIYKTSYPPDILLMKRSARNSCWKDAEYGLY 240

DB 181 FYIYSQTYERFQBEIKENTKNDKQMVQYIYKTSYPPDILLMKRSARNSCWKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 43

ADK72303

ID ADK72303 standard; protein; 281 AA.

XX ADK72303;

AC ADK72303;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human Apo-2 ligand with potential substitutions highlighted #1.

XX

KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;

KW variant; cancer; immune system disease; arthritis; multiple sclerosis;

KW human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 96

FT /note= "wild-type Ser may be substituted for Cys at this

FT location in the variant referred to in claim 1"

FT Misc-difference 101

FT /note= "wild-type Ser may be substituted for Cys at this

FT location in the variant referred to in claim 1"

FT Misc-difference 111

FT /note= "wild-type Ser may be substituted for Cys at this

FT location in the variant referred to in claim 1"

FT Misc-difference 170

FT /note= "wild-type Arg may be substituted for Cys at this

FT location in the variant referred to in claim 1"

FT Misc-difference 179

FT /note= "wild-type Lys may be substituted for Cys at this

FT location in the variant referred to in claim 1"

XX

XX WO2004001009-A2.

XX

XX 31-DEC-2003.

XX

XX 23-JUN-2003; 2003WO-US019750.

XX

XX 24-JUN-2002; 2002US-0391050P.

XX



QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 45  
ADK72296  
ID ADK72296 standard; protein; 281 AA.  
XX  
AC ADK72296;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human wild-type Apo-2 ligand, seq id 1.  
XX  
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
KW human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 119  
FT /note= "Encoded by CCN"  
XX  
PN WO2004001009-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 23-JUN-2003; 2003WO-US019750.  
XX  
PR 24-JUN-2002; 2002US-0391050P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Hymowitz S, Kelley RF, Lindstrom SH;  
XX  
DR WPI; 2004-082490/08.  
DR N-PSDB; ADK72297.  
XX  
PT New Apo-2 ligand variant polypeptide, useful for preparing a composition  
PT for treating cancer or immune-related disease, e.g., arthritis or  
PT multiple sclerosis.  
XX  
PS Claim 1; SEQ ID NO 1; 111pp; English.  
XX  
CC The invention relates to a novel isolated Apo-2 ligand variant  
CC polypeptide, comprising a sequence that differs from the native sequence  
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having  
CC one or more following amino acid substitutions at the residue positions  
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an  
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand  
CC variant polypeptide. Further disclosed are a composition comprising the  
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a  
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant  
CC polypeptide is useful for preparing a composition for treating cancer or  
CC immune-related disease, e.g., arthritis or multiple sclerosis. The  
CC current sequence represents the wild-type human Apo-2 ligand amino acid  
CC sequence.  
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLQSLCVAVTVYFTNELKQMDKYSKGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVITVLQSLCVAVTVYFTNELKQMDKYSKGIACFLKE 60  
QY 61 DSDYDPNDEESMNSPCWQVKQLROLVRKMLRTSEETISTVQEKQNNISPLVRRGPQ 120  
Db 61 DSDYDPNDEESMNSPCWQVKQLROLVRKMLRTSEETISTVQEKQNNISPLVRRGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHKG 180  
QY 181 FYIYISQTYFRFQREIKENTKNDKQMVQIYKYTSYPPDPILLMKSGARNSCWSDAEVGLY 240  
Db 181 FYIYISQTYFRFQREIKENTKNDKQMVQIYKYTSYPPDPILLMKSGARNSCWSDAEVGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281

RESULT 46  
ADK72310  
ID ADK72310 standard; protein; 281 AA.  
XX  
AC ADK72310;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human Apo-2 ligand with potential substitutions highlighted #3.  
XX  
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
KW human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 189  
FT /note= "wild-type Tyr may be substituted by Ala, Ser, Gln  
FT or Gly at this location in the variant referred to in  
FT claim 10"  
FT  
FT Misc-difference 191  
FT /note= "wild-type Arg may be substituted by Lys or Arg at  
FT this location in the variant referred to in claim 10"  
FT  
FT Misc-difference 193  
FT /note= "wild-type Gln may be substituted by Lys, Arg or  
FT Thr at this location in the variant referred to in claim  
FT 10"  
FT  
FT Misc-difference 264  
FT /note= "wild-type His may be substituted by Ala, His,  
FT Gly, Gln, Asp, Arg, Pro, Ser, Glu, Asn or Lys at this  
FT location in the variant referred to in claim 10"  
FT  
FT Misc-difference 266  
FT /note= "wild-type Ile may be substituted by Leu, Met or  
FT Val at this location in the variant referred to in claim  
FT 10"  
FT  
FT Misc-difference 267  
FT /note= "wild-type Asp may be substituted by Ser, Glu,  
FT Gln, Asp or Asn at this location in the variant referred  
FT to in claim 10"  
FT  
FT Misc-difference 269  
FT /note= "wild-type Asp may be substituted by Ser, Asn,  
FT Asp, Ala, Arg or Glu at this location in the variant  
FT referred to in claim 10"  
XX  
PN WO2004001009-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 23-JUN-2003; 2003WO-US019750.  
XX  
PR 24-JUN-2002; 2002US-0391050P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Hymowitz S, Kelley RF, Lindstrom SH;  
XX  
DR WPI; 2004-082490/08.  
XX

PT New Apo-2 ligand variant polypeptide, useful for preparing a composition  
PT for treating cancer or immune-related disease, e.g., arthritis or  
PT multiple sclerosis.

XX Claim 10; SEQ ID NO 1; 111pp; English.

XX The invention relates to a novel isolated Apo-2 ligand variant  
CC polypeptide, comprising a sequence that differs from the native sequence  
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having  
CC one or more following amino acid substitutions at the residue positions  
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an  
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand  
CC variant polypeptide. Further disclosed are a composition comprising the  
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a  
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant  
CC polypeptide is useful for preparing a composition for treating cancer or  
CC immune-related disease, e.g., arthritis or multiple sclerosis. The  
CC current sequence represents the human Apo-2 ligand amino acid sequence.  
CC Note: The variant sequence that is referred to in claim 10 may contain  
CC one or more of the potential substitutions highlighted in the features  
CC table for this record.

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVVYFTNKLQMDKYSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVVYFTNKLQMDKYSGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVKMTLRTSEETISTVQEKQNIPLVRERGPQ 120  
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVKMTLRTSEETISTVQEKQNIPLVRERGPQ 120  
QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
QY 181 FYYIYSQTYFRQBEIKENTKDKQWQVIYKYTSYDPDILLMKSNRSCSKDAEYGLY 240  
DB 181 FYYIYSQTYFRQBEIKENTKDKQWQVIYKYTSYDPDILLMKSNRSCSKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFSVTVNHEHLDMDHEASFFGAFVLG 281  
DB 241 SIYQGGIFELKENDRIFSVTVNHEHLDMDHEASFFGAFVLG 281

RESULT 47

ID ADJ63976 standard; protein; 281 AA.

XX AC ADJ63976;

XX 20-MAY-2004 (first entry)

XX Human apoptosis inducing molecule 1, AIM-1.

XX Human; apoptosis inducing molecule 1; AIM-1; apoptosis;  
KW autoimmune disease; graft versus host disease; lymphadenopathy;  
KW immunosuppressive; vasotropic; cytostatic; peripheral tolerance;  
KW cell activation; cell proliferation; immune regulation;  
KW inflammatory response; systemic lupus erythematosus;  
KW immunoproliferative disease; neoplasm; tumour; restenosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..38

FT /note= "signal peptide"

FT 39..281

FT /label= Mature\_AIM\_1

FT /note= "Claimed in claim 1"  
PN US2004038347-A1.

XX 26-FEB-2004.

XX 16-SEP-2003; 2003US-00662429.

XX 14-MAR-1996; 96US-0013405P.

PR 13-MAR-1997; 97US-00816981.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM;

PI WPI; 2004-203230/19.

DR N-PADB; ADJ63975.

XX Novel apoptosis inducing molecule polypeptide that induces apoptosis of  
PT cell line derived from pathological tissue and induces apoptosis of T  
PT cells, useful for treating lymphadenopathy, autoimmune diseases and graft  
PT versus host disease.

XX Claim 1; SEQ ID NO 2; 36pp; English.

XX The invention relates to apoptosis inducing molecule-I protein (AIM-I)  
CC comprising sequence that is 70 % identical to ADJ63976 or its mature form  
CC where the polypeptide binds antibody specific to AIM-1, induces apoptosis  
CC of cell line derived from pathological tissue and induces apoptosis of T  
CC cells. Also included are a composition comprising AIM-1 and a carrier,  
CC AIM-1 produced by a process involving expressing in a host cell a nucleic  
CC acid that encodes the protein so as to produce the protein (where the  
CC nucleic acid is chosen from a polynucleotide encoding AIM-1, mature AIM-  
CC 1, mature AIM-1 chosen for 1-5 or 5-10 conservative amino acid  
CC substitutions, the amino acid sequence encoded by human cDNA contained in  
CC ATCC deposit No. 97448, and a polynucleotide that is complementary to  
CC polynucleotide which hybridises at 60degreesC in a hybridisation buffer  
CC consisting of 0.5 X SSC (Saline-Sodium Citrate) and 0.1 % sodium dodecyl  
CC sulphate (SDS) to a polynucleotide chosen from polynucleotide encoding  
CC mature AIM-1, and a polynucleotide encoding amino acid sequence encoded  
CC by human cDNA contained in ATCC deposit No. 97448, where the  
CC polynucleotide encodes a polypeptide that has the same biological  
CC activity as described above). AIM-1 is useful for treating  
CC lymphadenopathy, autoimmune diseases, graft versus host disease, for  
CC stimulating peripheral tolerance, destroying pathologic transformed cell  
CC lines, mediating cell activation and proliferation. AIM-1 proteins are  
CC functionally linked as primary mediators of immune regulation and  
CC inflammatory response, are useful for diagnosis and treatment of  
CC disorders of cells, tissues and organisms. AIM-1 is useful as research  
CC tool in elucidating biology of autoimmune disorders including systemic  
CC lupus erythematosus, immunoproliferative disease lymphadenopathy and is  
CC useful for inhibiting neoplasia such as tumour cell growth. AIM-1 is also  
CC useful to treat diseases which required growth promotion activity e.g.,  
CC restenosis. AIM-1 is useful for assessing AIM-I binding capacity of its  
CC binding molecules such as receptor molecules. The present sequence  
CC represents AIM-1.

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVVYFTNKLQMDKYSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVVYFTNKLQMDKYSGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVKMTLRTSEETISTVQEKQNIPLVRERGPQ 120  
DB 61 DDSYWDPNDEESMNSPCQVKWQLRQLVKMTLRTSEETISTVQEKQNIPLVRERGPQ 120  
QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKG 180

Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180  
 QY 181 FYIISQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDILLMKSNRSCWSKDAEYGLY 240  
 Db 181 FYIISQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDILLMKSNRSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 48  
 ADL71816  
 ID ADL71816 standard; protein; 281 AA.  
 AC ADL71816;  
 DT 03-JUN-2004 (first entry)  
 DE Human apoptosis inducing molecule-I (AIM-I) protein.  
 XX  
 KW Apoptosis inducing molecule-I; AIM-I; cell activation;  
 KW cell differentiation; apoptosis; autoimmune disease;  
 KW graft-versus-host disease; lymphadenopathy; gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004047864-A1.  
 XX  
 PD 11-MAR-2004.  
 XX  
 PF 16-SEP-2003; 2003US-00662431.  
 XX  
 PR 14-MAR-1996; 96US-0013405P.  
 PR 13-MAR-1997; 97US-00816981.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM;  
 XX  
 DR WPI; 2004-226168/21.  
 DR N-PSDB; ADL71815.  
 XX  
 PT New antibodies specific to apoptosis inducing molecule I polypeptides  
 PT useful in research, biological, diagnostic, clinical or therapeutic  
 PT applications, such as in the treatment of autoimmune diseases or graft-  
 PT versus-host disease.  
 XX  
 PS Claim 1; SEQ ID NO 2; 36pp; English.  
 XX  
 CC The invention relates to antibodies specific to apoptosis inducing  
 CC molecule-I (AIM-I) polypeptides. The invention is useful in research,  
 CC biological, diagnostic, clinical or therapeutic applications. It is also  
 CC used for modulating activation and differentiation of cells, both  
 CC normally and in disease states, or for mediating apoptosis and preventing  
 CC or treating autoimmune diseases, graft-versus-host disease or  
 CC lymphadenopathy. The invention is also useful in gene therapy. The  
 CC present sequence is human AIM-I protein.  
 XX  
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVITVLQSLCVAVTVYFTNKLQKQDKYSGSIACFLKE 60  
 Db 1 MAMMEVQGGPSLGQTCVLIVITVLQSLCVAVTVYFTNKLQKQDKYSGSIACFLKE 60  
 QY 61 DDSYWDPNDESNWSPCWVKQLRQVRKMLRITSEETISTVQEQQNISPLVRERGPO 120  
 Db 61 DDSYWDPNDESNWSPCWVKQLRQVRKMLRITSEETISTVQEQQNISPLVRERGPO 120

QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180  
 Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG 180  
 QY 181 FYIISQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDILLMKSNRSCWSKDAEYGLY 240  
 Db 181 FYIISQTYFRQEEIKENTKNDKQMVQIYKYTSYDPDILLMKSNRSCWSKDAEYGLY 240  
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 49  
 ADK15498  
 ID ADK15498 standard; protein; 281 AA.  
 AC ADK15498;  
 DT 03-JUN-2004 (first entry)  
 DE Human TRAIL protein.  
 XX  
 KW Human; TRAIL; TNF related apoptosis inducing ligand; apoptosis;  
 KW cytostatic; virucide; tumour necrosis factor; Jurkat cell; cancer;  
 KW programmed cell death; leukaemia; colorectal cancer; viral infection;  
 KW vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..18 /note= "Cytoplasmic domain"  
 FT Domain 19..38 /note= "Transmembrane domain"  
 FT Domain 39..281 /note= "Extracellular domain claimed in claim 4"  
 FT Region 95..281 /note= "Claimed in claim 7"  
 FT  
 XX  
 PN US2004052788-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 02-SEP-2003; 2003US-00652244.  
 XX  
 PR 29-JUN-1995; 95US-00496632.  
 PR 01-NOV-1995; 95US-00548368.  
 PR 25-JUN-1996; 96US-00670354.  
 PR 26-MAR-1998; 98US-00048641.  
 PR 10-NOV-1998; 98US-00190046.  
 PR 26-MAY-1999; 99US-00320424.  
 PR 27-FEB-2001; 2001US-00796581.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Wiley SR, Goodwin RG;  
 XX  
 DR WPI; 2004-238577/22.  
 DR N-PSDB; ADK15497.  
 XX  
 PT New tumor necrosis factor related apoptosis inducing ligand polypeptides,  
 PT useful in studies of apoptosis, in regulating programmed cell death, or  
 PT for treating leukemia, cancer (e.g. colorectal cancer) or viral  
 PT infections.  
 XX  
 PS Claim 2; SEQ ID NO 2; 42pp; English.  
 XX  
 CC The invention relates to a new purified tumour necrosis factor related  
 CC apoptosis inducing ligand (TRAIL) polypeptide comprising an amino acid  
 CC sequence that is at least 90% identical to human TRAIL (ADK15498) or  
 CC mouse TRAIL (ADK15502). The TRAIL polypeptide induces apoptosis of Jurkat  
 CC cells. Also included are a purified human TRAIL polypeptide encoded by







KW	hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW	hyper-igm syndrome; hypohidrotic ectodermal dysplasia;
KW	X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW	viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW	viral replication; host cell survival; evasion of immune response;
KW	rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW	atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW	autoimmune disorder; hyper immune activity;
KW	aberrant acute phase response; hypercongenital condition; birth defect;
KW	neurotic lesion; wound; organ transplant rejection;
KW	aberrant signal transduction; proliferating disorder; cancer;
KW	HIV propagation; human.
XX	
OS	Homo sapiens.
XX	
PN	WO2004065577-A2.
XX	
PD	05-AUG-2004.
XX	
PF	13-JAN-2004; 2004WO-US0000798.
XX	
XX	14-JAN-2003; 2003US-0440068P.
PR	
PR	12-MAY-2003; 2003US-0469757P.
PR	
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Nadler SG, Neubauer MG, Feder JN, Carman J;
XX	
DR	WPI; 2004-562168/54.
DR	N-PSDB; ADR14208.
PT	
PT	New isolated polynucleotides and polypeptides associated with NF-kappaB
PT	pathway, useful for diagnosing, treating, or preventing disorders or
PT	diseases associated with NF-kappaB pathway.
PS	Claim 6; SEQ ID NO 210; 237pp; English.
XX	
CC	This invention relates to the novel association of protein sequences (and
CC	the genes which encode them) to the NF-kappaB pathway. The invention may
CC	be useful for the production of compounds with an anti-inflammatory,
CC	cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
CC	gastrointestinal-gen, antiasthmatic, antiarteriosclerotic,
CC	immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
CC	vulnerable activity or for gene therapy. The proteins and nucleotides are
CC	useful for diagnosing, preventing, treating, or ameliorating conditions
CC	or diseases associated with the NF-kappaB pathway. The condition is an
CC	immune disorder, an inflammatory disorder, an inflammatory disorder
CC	related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
CC	hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-igm
CC	syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
CC	ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
CC	hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
CC	survival, evasion of immune responses, rheumatoid arthritis, inflammatory
CC	bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
CC	syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
CC	immune activity, disorders related to aberrant acute phase responses,
CC	hypercongenital conditions, birth defects, necrotic lesions, wounds,
CC	organ transplant rejection, conditions related to organ transplant
CC	rejection, disorders related to aberrant signal transduction,
CC	proliferating disorders, cancers and HIV propagation in cells infected
CC	with other viruses. The present sequence is that of a human protein which
CC	is subject to the novel association with the NF-kappaB pathway of the
CC	invention. Note: This sequence does not appear in the specification but
CC	was obtained by the indexer from Genbank.
XX	
SQ	Sequence 281 AA;
	Query Match 100.0%; Score 281; DB 8; Length 281;
	Best Local Similarity 100.0%; Pred. No. 2.9e-266;
	Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 MAMMEYQGGSIGQTCVLIVIFVTLLOSGLCAVTVYFTNELKOMQDKYSKSGIACFLKE 60

1	Db	1	MAMVEVQGGPSLGQTCVLIVITVLLQSLCAVTVYVPTNELKQMDQKYSKSGIACFLKE	60
61	Qy	61	DDSYDPNDDESMSPCQVQKWQLRQLVRKMLITSEETISTVQEKQOINTSPLVRERGPQ	120
61	Db	61	DDSYDPNDDESMSPCQVQKWQLRQLVRKMLITSEETISTVQEKQOINTSPLVRERGPQ	120
121	Qy	121	RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVLVTHEKG	180
121	Db	121	RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVLVTHEKG	180
181	Qy	181	FYYIYSQTYFRFQBEIKENTKNDQMQVQIYKYTSPDPIILLMKSAENSCWSKDAEYGLY	240
181	Db	181	FYYIYSQTYFRFQBEIKENTKNDQMQVQIYKYTSPDPIILLMKSAENSCWSKDAEYGLY	240
241	Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPFLVG	281
241	Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPFLVG	281

RESULT 52	
ADK82215	
ID	ADK82215 standard; protein; 281 AA.
XX	
AC	ADK82215;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Human TRAIL amino acid sequence SEQ ID NO:66.
XX	
KW	antibody; VH domain; VL domain; TR4 binding antibody; TRAIL receptor;
KW	haematological cancer; cytostatic; immunotherapy; Non-Hodgkin's lymphoma;
KW	chronic myelogenous lymphoma; multiple myeloma;
KW	chronic lymphocytic leukaemia; scfv; human; TRAIL;
KW	TNF-related apoptosis-inducing ligand.
XX	
OS	Homo sapiens.
XX	
PN	WO2004016753-A2.
XX	
PD	26-FEB-2004.
XX	
PF	15-AUG-2003; 2003WO-US025457.
XX	
PR	15-AUG-2002; 2002US-0403382P.
PR	13-NOV-2002; 2002US-0425730P.
PR	06-MAY-2003; 2003US-0468050P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Salcedo T, Ruben SM, Rosen CA, Albert VA;
XX	
DR	WPI; 2004-203784/19.

```

SQ      Sequence 281 AA;

Query Match      100.0%; Score 281; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.9e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1 MAMMEVQGSPSLGQTCVLIVIFVTLLOSGLCAVTVYFTNELKOMQDKYSKGIACPLKE 60
      |||||

```

CC Hodgkin's lymphoma, chronic myelogenous lymphoma, multiple myeloma, or  
CC chronic lymphocytic leukaemia. The present sequence represents human  
CC tumour necrosis factor (TNF) related apoptosis-inducing ligand (TRAIL),  
CC which is used in the exemplification of the present invention.

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDPILLMKSARNCSWSDAEYGLY 240

DB 181 FYYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDPILLMKSARNCSWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 53

ADS88000  
ID ADS88000 standard; protein; 281 AA.

AC ADS88000;

DT 18-NOV-2004 (first entry)

DE Tumour treatment-related human protein sequence SeqID36.

XX tumour inhibition; tumour treatment; metastasis; infectious lesion;  
KW antigen presenting cell; immunostimulatory cytokine; cytostatic;  
KW vulnery; immunomodulator; melanoma; hepatoma; adenocarcinoma;  
KW colorectal cancer; basal cell cancer; oral cancer; nasopharyngeal cancer;  
KW laryngeal cancer; bladder cancer; head cancer; neck cancer;  
KW renal cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer;  
KW ovarian cancer; oesophageal cancer; gastric cancer; prostate cancer;  
KW testicular cancer; breast cancer; human.

OS Homo sapiens.

XX WO2004034995-A2.

PN 29-APR-2004.

XX 15-OCT-2003; 2003WO-US032827.

XX 15-OCT-2002; 2002US-0418865P.

XX (UYPI-) UNIV PITTSBURGH.

XX Lotze MT, Tahara H;

XX WPI; 2004-365083/34.

DR N-PSDB; ADS87999.

XX Inhibiting or treating a tumor, metastasis or infectious lesion comprises  
PT administering into or near site of a tumor or infectious lesion an  
PT antigen presenting cell and an immunostimulatory cytokine or a nucleic  
PT acid encoding the cytokine.

PS Disclosure; SEQ ID NO 36; 169pp; English.  
XX This invention relates to a novel method of inhibiting or treating a  
CC tumour, metastasis or infectious lesion in a subject which comprises  
CC administering into or near a site of a tumour or infectious lesion in a  
CC subject an antigen presenting cell and an immunostimulatory cytokine or a  
CC nucleic acid encoding the cytokine. The invention may be useful for the  
CC production of compounds with a cytostatic or vulnery activity acting as  
CC immunomodulators. The method is useful in inhibiting or treating a  
CC tumour, metastasis or infectious lesion in a subject, where the size of  
CC the tumour, metastasis (where number is also decreased) or infectious  
CC lesion is decreased. The tumour is selected from melanoma, hepatoma,  
CC adenocarcinoma, colorectal cancer, basal cell cancer, oral cancer,  
CC nasopharyngeal cancer, laryngeal cancer, bladder cancer, head and neck  
CC cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical  
CC cancer, ovarian cancer, oesophageal cancer, gastric cancer, prostate  
CC cancer, testicular cancer and breast cancer. The present sequence is that  
CC of a protein which is related to the invention.

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180

QY 181 FYYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDPILLMKSARNCSWSDAEYGLY 240

DB 181 FYYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYPPDPILLMKSARNCSWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 54

AB084415  
ID AB084415 standard; protein; 281 AA.

XX AB084415;

DT 18-NOV-2004 (first entry)

XX Human cancer-associated protein HP7-053.3.

DE Human cancer-associated protein; cytostatic; cancer; leukaemia;  
KW lymphoma; CAP.

XX Homo sapiens.

XX WO2004074320-A2.

XX 02-SEP-2004.

PD 17-FEB-2004; 2004WO-US004730.

XX 14-FEB-2003; 2003US-00367094.

XX 14-MAR-2003; 2003US-00388838.

XX 15-APR-2003; 2003US-00417375.

XX 13-JUN-2003; 2003US-00461862.

XX 15-SEP-2003; 2003US-00663431.

XX 15-DEC-2003; 2003US-00737318.

XX (SAGR-) SAGRES DISCOVERY INC.  
XX Morris DW, Morris DW, Malandro MS;  
XX WPI: 2004-652914/63.  
XX N-PSDB; ABD32555.  
XX New isolated cancer-associated polynucleotides and polypeptides useful  
PT for diagnosing, preventing or treating cancers, especially lymphoma and  
PT leukemia, or in screening for agents that modulate cancer.  
XX claim 18; seqid 36; 310pp; English.  
XX The invention relates to an isolated nucleic acid comprising at least 10  
CC contiguous nucleotides of any of the 233 polynucleotide sequences given  
CC in the specification, or its complement. The nucleic acids encode cancer-  
CC associated proteins. Also included are an expression vector comprising  
CC the isolated nucleic acid cited above, a host cell comprising the above  
CC recombinant nucleic acid or expression vector, a microarray for detecting  
CC a cancer-associated (CA) nucleic acid comprising at least one probe  
CC comprising at least 10 contiguous nucleotides of any of the above-  
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within  
CC an open reading frame of a CA sequence selected from any of the 95  
CC polynucleotide sequences as mentioned in the specification, or its  
CC complement), an isolated antibody, (or its antigen binding fragment) that  
CC binds to the above polypeptide, a hybridoma that produces the above  
CC monoclonal antibody, a pharmaceutical composition comprising the above  
CC antibody and a pharmaceutical excipient, a kit for detecting cancer  
CC cells (comprising the antibody cited above, methods for diagnosing cancer  
CC or for detecting the presence or absence of cancer cells in an  
CC individual, a method for inhibiting growth of cancer cells in an  
CC individual, a method for delivering a therapeutic agent to cancer cells  
CC in an individual, an electronic library comprising the above  
CC polynucleotide or polypeptide (or their fragments), methods of screening  
CC for anticancer activity or for a bioactive agent capable of modulating  
CC the activity of a CA protein (CAP), methods for detecting cancer  
CC associated with expression of a polypeptide in a test cell sample, a  
CC method for treating cancers and a method for inhibiting the expression of  
CC CA gene in a cell. The composition and methods are useful for detecting,  
CC diagnosing, preventing and treating cancers, especially lymphoma and  
CC leukaemia. These may also be used in screening for agents that modulate  
CC cancer. The present sequence is a human CAP protein sequence. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 281 AA;  
SQ  
Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVITVLQSLCVAVTVYFTNELKQMDKYSGKGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVITVLQSLCVAVTVYFTNELKQMDKYSGKGIACFLKE 60  
QY 61 DSDYNDPNDDESMNPGCWKKQLROLVRKMLRTSEETISTVQEQQNISPVLVRERGPO 120  
DB 61 DSDYNDPNDDESMNPGCWKKQLROLVRKMLRTSEETISTVQEQQNISPVLVRERGPO 120  
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180  
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHEKG 180  
QY 181 FYIYISQTYFRQEEIKENTKDKQKVYIYKTSYDPDILLMKSNRSCWDAEYGLY 240  
DB 181 FYIYISQTYFRQEEIKENTKDKQKVYIYKTSYDPDILLMKSNRSCWDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 55  
ADP23388  
ID ADP23388 standard; protein; 281 AA.  
XX  
AC ADP23388;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE PRO polypeptide SEQ ID NO:566.  
XX  
KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;  
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;  
KW antiaschmatic; hepatotropic; respiratory; gene therapy; immune system.  
XX Unidentified.  
XX WO2004041170-A2.  
XX  
PD 21-MAY-2004.  
XX  
PF 30-OCT-2003; 2003WO-US034312.  
XX  
PR 01-NOV-2002; 2002US-0423394P.  
XX (GETH ) GENENTECH INC.  
PA Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
PI Wu TD;  
XX  
DR WPI: 2004-419628/39.  
DR N-PSDB; ADP23387.  
XX  
PT New PRO polypeptides and polynucleotides, useful for treating e.g.  
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
PT renal disease, or demyelinating diseases of the central or peripheral  
PT nervous system.  
XX  
PS Claim 7; SEQ ID NO 566; 2940pp; English.  
XX  
CC The invention relates to a novel isolated nucleic acid and the PRO  
CC polypeptide encoded by it. A protein of the invention has  
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
CC antiaschmatic, hepatotropic, and respiratory activity. A polynucleotide  
CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
CC agonist, antagonist, or antibody that specifically binds to the  
CC polypeptide is useful for treating an immune related disorder such as  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
CC disease, a demyelinating disease of the central or peripheral nervous  
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
CC disease, infectious or autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
CC hypersensitivity, urticaria, an immunologic disease of the lung,  
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence represents a PRO protein  
CC of the invention.  
XX  
SQ Sequence 281 AA;  
Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-266;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAMMEVQGGPSLG	QTVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYKSGIACFLKE	60
Db	1	MAMMEVQGGPSLG	QTVLIVFTVLLQSLCVAVTYYVFTNELKQMDKYKSGIACFLKE	60
Qy	61	DDSYWDPNDDESMNSPC	QWQKWLRLVRYKMLILRTSEETISTVQEKQNIISPLVRGPQ	120
Db	61	DDSYWDPNDDESMNSPC	QWQKWLRLVRYKMLILRTSEETISTVQEKQNIISPLVRGPQ	120
Qy	121	RVAAHITGTRGSRNTL	SSPNSKNEALGRKINSWESSRSGHSFNLNHLRNGELVIHEKG	180
Db	121	RVAAHITGTRGSRNTL	SSPNSKNEALGRKINSWESSRSGHSFNLNHLRNGELVIHEKG	180
Qy	181	FYYIYSQTYFRFQBEI	KNTKNDKQMVQIYKYTSYDPDILLMKSRNSCWSKDAEYGLY	240
Db	181	FYYIYSQTYFRFQBEI	KNTKNDKQMVQIYKYTSYDPDILLMKSRNSCWSKDAEYGLY	240
Qy	241	SIYQGGIFELKENDRI	FVSVTNEHLIDMDHEASFFGAFLVG	281
Db	241	SIYQGGIFELKENDRI	FVSVTNEHLIDMDHEASFFGAFLVG	281
RESULT	56			
ID	ADN95444			
XX	ADN95444	standard; protein; 280 AA.		
XX	AC	ADN95444;		
XX	AC	ADN95444;		
DT	01-JUL-2004	(first entry)		
XX	XX	Human BEC/LEC-related protein sequence SeqID367.		
DE	XX	Growth; differentiation; blood endothelial cell; BEC;		
KW	KW	lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;		
KW	KW	lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;		
KW	KW	vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;		
KW	KW	inflammatory disease; cancer metastasis; lymphatic system; human.		
XX	XX			
OS	XX	Homo sapiens.		
XX	XX			
PN	XX	WO2003080640-A1.		
XX	XX			
PD	XX	02-OCT-2003.		
PF	XX			
PF	XX	07-MAR-2003; 2003WO-US006900.		
XX	XX			
PR	XX	07-MAR-2002; 2002US-0363019P.		
XX	XX			
PA	XX	(LUDW-) LUDWIG INST CANCER RES.		
PA	XX	(LICN) LICENTIA LTD.		
PI	XX			
PI	XX	Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;		
XX	XX			
DR	XX	WPI; 2003-876899/81.		
DR	XX	N-PSDB; ADN95445.		
PS	XX			
PS	XX	Example 1; SEQ ID NO 367; 176pp; English.		
XX	XX			
CC	XX	This invention relates to a method of differentially modulating the		
CC	XX	growth or differentiation of blood endothelial cells (BEC) or lymphatic		
CC	XX	endothelial cells (LEC) comprises contacting endothelial cells with a		
CC	XX	composition comprising an agent that differentially modulates blood or		
CC	XX	lymphatic endothelial cells. Treating hereditary lymphoedema comprises		
CC	XX	identifying a human subject with lymphoedema and with a mutation in at		
CC	XX	least one allele of a gene encoding a LEC protein, where the mutation		
CC	XX	correlates with lymphoedema in human subjects, and with the proviso that		
CC	XX	the LEC protein is not VEGFR-3; and administering to the subject a		
CC	XX	composition comprising a lymphatic growth agent selected from VEGF-C or		
CC	XX	VEGF-D polypeptides and polynucleotides. The invention may be useful for		
CC	XX	the development of compounds with an antiangiogenic, cytostatic,		
CC	XX	vasotropic or antiinflammatory activity or for gene therapy. The method		
CC	XX	is useful in modulating the growth or differentiation of blood		
CC	XX	endothelial cells or lymphatic endothelial cells, in treating hereditary		

DR WPI; 1998-497862/43.  
 XX New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent  
 PT and treat e.g. inflammation, arthritis, septicemia, autoimmune diseases,  
 PT infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,  
 PT AIDS and bone diseases.  
 XX  
 PS Disclosure; Page 17-18; 22pp; English.  
 XX  
 CC This is the amino acid sequence of human TL2 (also known as TRAIL), which  
 CC has newly been discovered to be a ligand of human tumour necrosis related  
 CC receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and  
 CC TL2 can be used in screening processes for compounds which bind the  
 CC receptor, or its ligand, and which activate (agonists) or inhibit  
 CC (antagonists) the receptor or TL2. Treatment of a subject with the need  
 CC to inhibit TR5 polypeptide activity comprises administering an antagonist  
 CC to the polypeptide, administering a nucleic acid that inhibits the  
 CC expression of the nucleotide sequence encoding the polypeptide and/or  
 CC administering a polypeptide that competes with the polypeptide for its  
 CC ligand, substrate or receptor. The active agents can be used for the  
 CC treatment of chronic and acute inflammation, arthritis, septicemia,  
 CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),  
 CC transplant rejection, graft vs host disease, infection, stroke,  
 CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,  
 CC AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),  
 CC atherosclerosis and Alzheimer's disease  
 XX  
 SQ Sequence 279 AA;  
 Query Match 99.3%; Score 279; DB 2; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-264;  
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKEDD 62  
 DB 1 MMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKEDD 60  
 QY 63 SYWDNDEESMNSPCQVQWQLRQLVRKMLRTSETISTVQEKQNIPLVREGRQVR 122  
 DB 61 SYWDNDEESMNSPCQVQWQLRQLVRKMLRTSETISTVQEKQNIPLVREGRQVR 120  
 QY 123 AAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGFY 182  
 DB 121 AAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGFY 180  
 QY 183 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLYSI 242  
 DB 181 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLYSI 240  
 QY 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
 DB 241 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 279  
 RESULT 58  
 AAW95032  
 ID AAW95032 standard; protein; 279 AA.  
 XX  
 AC AAW95032;  
 XX  
 DT 13-MAY-1999 (first entry)  
 XX  
 DE Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.  
 XX  
 KW Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;  
 KW inflammation; septicemia; autoimmune disease; transplant rejection;  
 KW Graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;  
 KW acute respiratory disease syndrome; restenosis; bone disease; cancer;  
 KW atherosclerosis; Alzheimer's disease.  
 OS Unidentified.  
 XX  
 FN EP897114-A2.

XX 17-FEB-1999.  
 XX 04-JUN-1998; 98EP-00304424.  
 XX 13-AUG-1997; 97US-0055513P.  
 PR 26-AUG-1997; 97US-0056980P.  
 PR 29-AUG-1997; 97US-0057550P.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA Brigham-Burke MR, Young PR;  
 XX WPI; 1999-134308/12.  
 XX  
 PT Identifying agonists and antagonists to tumour necrosis factor receptor  
 PT (TNF-R) related polypeptides (LR1, LR2, LR2 and LR4) - useful for  
 PT treating stroke, Alzheimer's disease and AIDS.  
 XX  
 PS Disclosure; Page 14-15; 18pp; English.  
 XX  
 CC The invention relates to identifying agonists or antagonists to tumour  
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2  
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a  
 CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2  
 CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)  
 CC assessing the ability of the candidate compound to compete with TR1 or  
 CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful  
 CC for treating diseases caused by imbalance of TL or TR polypeptide levels,  
 CC which cause: chronic and acute inflammation, arthritis, septicemia,  
 CC autoimmune diseases, transplant rejection, graft vs. host disease,  
 CC infection, stroke, ischemia, acute respiratory disease syndrome,  
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and  
 CC Alzheimer's disease. The present sequence represents a TNF-R related  
 CC polypeptide TL2  
 XX  
 SQ Sequence 279 AA;  
 Query Match 99.3%; Score 279; DB 2; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-264;  
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKEDD 62  
 DB 1 MMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKEDD 60  
 QY 63 SYWDNDEESMNSPCQVQWQLRQLVRKMLRTSETISTVQEKQNIPLVREGRQVR 122  
 DB 61 SYWDNDEESMNSPCQVQWQLRQLVRKMLRTSETISTVQEKQNIPLVREGRQVR 120  
 QY 123 AAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGFY 182  
 DB 121 AAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGFY 180  
 QY 183 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLYSI 242  
 DB 181 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLYSI 240  
 QY 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
 DB 241 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 279  
 RESULT 59  
 AAY27018  
 ID AAY27018 standard; protein; 281 AA.  
 XX  
 AC AAY27018;  
 XX  
 DT 24-SEP-1999 (first entry)  
 XX  
 DE Human Apo-2 ligand (Apo-2L) variant D269A.  
 XX

Query Match	95.4%	Score 268	DB 2	Length 281
Best Local Similarity	100.0%	Pred. No. 1.5e-253		
Matches 268	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYKSGIACFLKE	60	
Db	1	MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYKSGIACFLKE	60	
Qy	61	DDSYWDPNDESMNSPCQVQVKQLRQLVKMTLRTSEETISVQKQKQNIISPLVRRGQP	120	
Db	61	DDSYWDPNDESMNSPCQVQVKQLRQLVKMTLRTSEETISVQKQKQNIISPLVRRGQP	120	
Qy	121	RVAAHITTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG	180	
Db	121	RVAAHITTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG	180	
Qy	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSPDPILLMKGARNSCWSKDAEYGLY	240	
Db	181	FYYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSPDPILLMKGARNSCWSKDAEYGLY	240	
Qy	241	SIYOGGIFELKENDRIFVSVTNEHLIDM	268	
Db	241	SIYOGGIFELKENDRIFVSVTNEHLIDM	268	

RESULT 60

ADB61495  
ID ADB61495 standard; protein; 281 AA.  
XX  
XX ADB61495;  
XX  
XX  
DT 04-DEC-2003 (first entry)  
XX  
XX Human Apo-2 ligand protein mutant H264C.  
XX  
XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;  
KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;  
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;  
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;  
KW human; mutant; mutein.  
XX  
XX Synthetic.  
OS Homo sapiens.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 264  
FT /note= "Native residue of His is substituted by Cys"  
XX  
XX W02003029420-A2.  
BN  
XX  
XX 10-APR-2003.  
PD  
XX  
XX 01-OCT-2002; 2002WO-US031210.  
XX  
XX 02-OCT-2001; 2001US-0326622P.  
PR  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Kelley RF, Lindstrom SH;  
PI  
XX  
XX WFI; 2003-541400/51.  
XX  
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating  
PT cancer or an immune-related disease such as multiple sclerosis, comprises  
PT amino acid substitutions in the native sequence of the Apo-2 ligand.  
XX  
XX  
PS Claim 1; Page; 92pp; English.  
XX  
XX The invention relates to a novel isolated Apo-2 ligand variant  
CC polypeptide having a sequence that differs from the native sequence  
CC having 281 amino acids given in specification. The Apo-2 ligand variant  
CC polypeptide is selected from a polypeptide having substitutions at  
CC residue positions identified from x-ray crystal structure of the  
CC DR5.Apo2L complex. The polypeptide having the substitutions made at  
CC residue position(s) selected from 20 positions such as S96C, S101C,  
CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,  
CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the  
CC residue position is, outside of the receptor contact region of the  
CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal  
CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide  
CC and further compositions have the following activities: cytostatic,  
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,  
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for  
CC inducing apoptosis in mammalian cells, by exposing mammalian cells  
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a  
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,  
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are  
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,  
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for  
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an  
CC immune-related disease (such as arthritis or multiple sclerosis) in a  
CC mammal, by administering to the mammal an effective amount of the Apo-2  
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand  
CC trimer. This sequence represents the human Apo-2 ligand mutant H264C  
CC protein of the invention. NOTE: This sequence is not shown in the  
CC specification. It has been created from information provided in claim 1  
CC and from the sequence in Fig 1 of the specification.  
XX  
SQ Sequence 281 AA;



Query Match 93.6%; Score 263; DB 7; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-246;  
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYNDPDEESMNSPCWQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120  
 DB 61 DDSYNDPDEESMNSPCWQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHPSFLNLHRLNGELVTHEKG 180  
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHPSFLNLHRLNGELVTHEKG 180

QY 181 FYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240  
 DB 181 FYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNE 263  
 DB 241 SIYQGGIFELKENDRIFVSVTNE 263

RESULT 61  
 ADB61494  
 ID ADB61494 standard; protein; 281 AA.  
 AC ADB61494;  
 XX  
 DT 04-DEC-2003 (first entry)  
 DE Human Apo-2 ligand protein mutant E263C.  
 KW Apo-2 ligand; DR5-Apo2L complex; receptor contact region;  
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;  
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;  
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;  
 KW human; mutant; mutein.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 FH Key  
 FT Location/Qualifiers  
 FT Misc-difference 263 /note= "Native residue of Glu is substituted by Cys"  
 FT  
 XX WO2003029420-A2.  
 PN 10-APR-2003.  
 XX  
 XX 01-OCT-2002; 2002WO-US031210.  
 XX  
 XX 02-OCT-2001; 2001US-0326622P.  
 PR  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Kelley RF, Lindstrom SH;  
 PI  
 XX WPI; 2003-541400/51.  
 DR  
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating  
 PT cancer or an immune-related disease such as multiple sclerosis, comprises  
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.  
 XX  
 XX Claim 1; Page; 92pp; English.  
 PS  
 XX The invention relates to a novel isolated Apo-2 ligand variant  
 CC polypeptide having a sequence that differs from the native sequence  
 CC having 281 amino acids given in specification. The Apo-2 ligand variant  
 CC polypeptide is selected from a polypeptide having substitutions at

CC residue positions identified from x-ray crystal structure of the  
 CC DR5-Apo2L complex. The polypeptide having the substitutions made at  
 CC residue position(s) selected from 20 positions such as S96C, S101C,  
 CC S111C, V114C, R115C, E116C, N134C, R140C, E144C, N152C, S153C, R170C,  
 CC R170K, R170S, K179C, D234C, R249C, R255C, E263C, H264C, such that the  
 CC residue position is, outside of the receptor contact region of the  
 CC DR5-Apo2L complex, and displays high solvent accessibility in the crystal  
 CC structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide  
 CC and further compositions have the following activities: cytostatic,  
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,  
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for  
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells  
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a  
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,  
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are  
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,  
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for  
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an  
 CC immune-related disease (such as arthritis or multiple sclerosis) in a  
 CC mammal, by administering to the mammal an effective amount of the Apo-2  
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand  
 CC trimer. This sequence represents the human Apo-2 ligand mutant E263C  
 CC protein of the invention. NOTE: This sequence is not shown in the  
 CC specification. It has been created from information provided in claim 1  
 CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 93.2%; Score 262; DB 7; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-247;  
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYNDPDEESMNSPCWQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120  
 DB 61 DDSYNDPDEESMNSPCWQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQ 120

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHPSFLNLHRLNGELVTHEKG 180  
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHPSFLNLHRLNGELVTHEKG 180

QY 181 FYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240  
 DB 181 FYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTN 262  
 DB 241 SIYQGGIFELKENDRIFVSVTN 262

RESULT 62

ADB61493

ID ADB61493 standard; protein; 281 AA.

XX

AC ADB61493;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human Apo-2 ligand protein mutant R255C.

XX Apo-2 ligand; DR5-Apo2L complex; receptor contact region;

KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;

KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;

KW lung; breast; immune-related disease; arthritis; multiple sclerosis;

KW human; mutant; mutein.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key

Location/Qualifiers

FT Misc-difference 255 /note= "Native residue of Arg is substituted by Cys"  
XX WO2003029420-A2.  
XX PD 10-APR-2003.  
XX PF 01-OCT-2002; 2002WO-US031210.  
XX PR 02-OCT-2001; 2001US-0326622P.  
XX XX (GETH ) GENENTECH INC.  
XX PI Kelley RF, Lindstrom SH;  
XX XX WPI; 2003-541400/51.  
XX DR Novel isolated Apo-2 ligand variant polypeptide useful for treating  
XX cancer or an immune-related disease such as multiple sclerosis, comprises  
XX amino acid substitutions in the native sequence of the Apo-2 ligand.  
XX Claim 1; Page; 92pp; English.  
XX The invention relates to a novel isolated Apo-2 ligand variant  
XX polypeptide having a sequence that differs from the native sequence  
XX having 281 amino acids given in specification. The Apo-2 ligand variant  
XX polypeptide is selected from a polypeptide having substitutions at  
XX residue positions identified from x-ray crystal structure of the  
XX DR5-Apo2L complex. The polypeptide having the substitutions made at  
XX residue position(s) selected from 20 positions such as S96C, S101C,  
XX S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C,  
XX R170K, R170S, K179C, D234C, E249C, R255C, H264C, such that the  
XX residue position is, outside of the receptor contact region of the  
XX DR5-Apo2L complex, and displays high solvent accessibility in the crystal  
XX structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide  
XX and further compositions have the following activities: cytostatic,  
XX antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,  
XX an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for  
XX inducing apoptosis in mammalian cells, by exposing mammalian cells  
XX expressing a receptor selected from DR4 receptor and DR5 receptor to a  
XX therapeutically effective amount of the Apo-2 ligand variant polypeptide,  
XX Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are  
XX colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,  
XX the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for  
XX treating cancer (such as lung, breast, colon or colorectal cancer) or an  
XX immune-related disease (such as arthritis or multiple sclerosis) in a  
XX mammal, by administering to the mammal an effective amount of the Apo-2  
XX ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand  
XX trimer. This sequence represents the human Apo-2 ligand mutant R255C  
XX protein of the invention. NOTE: This sequence is not shown in the  
XX specification. It has been created from information provided in claim 1  
XX and from the sequence in Fig 1 of the specification.

Query Match 90.4%; Score 254; DB 7; Length 281;  
Best Local Similarity 100.0%; Pred. No. 7.6e-240;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVGGPSLGQTCVLIVFTVLQSLCAVTVYFTNELKQMDKYKSGIACFLKE 60  
DB 1 MAMVEVGGPSLGQTCVLIVFTVLQSLCAVTVYFTNELKQMDKYKSGIACFLKE 60  
QY 61 DSDYWDNDDESMNSPCWQVKQLVRKMLRTSEETISTVQEQQNISPLVRRGPQ 120  
DB 61 DSDYWDNDDESMNSPCWQVKQLVRKMLRTSEETISTVQEQQNISPLVRRGPQ 120  
QY 121 RVAAHITGRGNTLSSPNSKNEALGRKINSWESSRSGHFLSNLNLRLNGELVIHKG 180  
DB 121 RVAAHITGRGNTLSSPNSKNEALGRKINSWESSRSGHFLSNLNLRLNGELVIHKG 180  
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240  
DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240

Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSKDAEYGLY 240  
QY 241 SIYOGGIFELKEND 254  
DB 241 SIYOGGIFELKEND 254  
RESULT 63  
ADB61492  
ID ADB61492 standard; protein; 281 AA.  
XX ADB61492;  
XX 04-DEC-2003 (first entry)  
XX Human Apo-2 ligand protein mutant E249C.  
XX Apo-2 ligand; DR5-Apo2L complex; receptor contact region;  
XX high solvent accessibility; cytostatic; antiarthritic; neuroprotective;  
XX trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;  
XX lung; breast; immune-related disease; arthritis; multiple sclerosis;  
XX human; mutant; mutein.  
XX Synthetic.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FT Misc-difference 249 /note= "Native residue of Glu is substituted by Cys"  
XX WO2003029420-A2.  
XX 10-APR-2003.  
XX 01-OCT-2002; 2002WO-US031210.  
XX 02-OCT-2001; 2001US-0326622P.  
XX (GETH ) GENENTECH INC.  
XX Kelley RF, Lindstrom SH;  
XX WPI; 2003-541400/51.  
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating  
XX cancer or an immune-related disease such as multiple sclerosis, comprises  
XX amino acid substitutions in the native sequence of the Apo-2 ligand.  
XX Claim 1; Page; 92pp; English.  
XX The invention relates to a novel isolated Apo-2 ligand variant  
XX polypeptide having a sequence that differs from the native sequence  
XX having 281 amino acids given in specification. The Apo-2 ligand variant  
XX polypeptide is selected from a polypeptide having substitutions at  
XX residue positions identified from x-ray crystal structure of the  
XX DR5-Apo2L complex. The polypeptide having the substitutions made at  
XX residue position(s) selected from 20 positions such as S96C, S101C,  
XX S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C,  
XX R170K, R170S, K179C, D234C, E249C, R255C, H264C, such that the  
XX residue position is, outside of the receptor contact region of the  
XX DR5-Apo2L complex, and displays high solvent accessibility in the crystal  
XX structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide  
XX and further compositions have the following activities: cytostatic,  
XX antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,  
XX an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for  
XX inducing apoptosis in mammalian cells, by exposing mammalian cells  
XX expressing a receptor selected from DR4 receptor and DR5 receptor to a  
XX therapeutically effective amount of the Apo-2 ligand variant polypeptide,  
XX Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are  
XX colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,  
XX the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for  
XX treating cancer (such as lung, breast, colon or colorectal cancer) or an  
XX immune-related disease (such as arthritis or multiple sclerosis) in a  
XX mammal, by administering to the mammal an effective amount of the Apo-2  
XX ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand  
XX trimer. This sequence represents the human Apo-2 ligand mutant R255C  
XX protein of the invention. NOTE: This sequence is not shown in the  
XX specification. It has been created from information provided in claim 1  
XX and from the sequence in Fig 1 of the specification.



CC mammal, by administering to the mammal an effective amount of the Apo-2  
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand  
 CC trimer. This sequence represents the human Apo-2 ligand mutant E249C  
 CC protein of the invention. NOTE: This sequence is not shown in the  
 CC specification. It has been created from information provided in claim 1  
 CC and from the sequence in Fig 1 of the specification.  
 XX  
 SQ Sequence 281 AA;

Query Match 88.3%; Score 248; DB 7; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-234;  
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120  
 DB 61 DSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120  
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
 QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYPPDPILLMKSARNCSWKDAEYGLY 240  
 DB 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYPPDPILLMKSARNCSWKDAEYGLY 240  
 QY 241 SIYQGI 248  
 DB 241 SIYQGI 248

RESULT 64  
 AA01516  
 ID AA01516 standard; peptide; 281 AA.  
 AC AA01516;  
 XX  
 DT 27-MAY-1999 (first entry)  
 DE Protein associated with neurodegenerative and autoimmune diseases.  
 XX  
 KW Neurodegenerative disease; autoimmune disease; inflammatory disease;  
 KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;  
 KW surface receptor; TRAIL protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 245 /note= "Gly or Cys"  
 FT  
 XX  
 PN FR2766713-Al.  
 PD 05-FEB-1999.  
 XX  
 PF 04-AUG-1997; 97FR-00010176.  
 PR 04-AUG-1997; 97FR-00010176.  
 XX  
 PA (INMR ) BIO MERIEUX.  
 PI Rieger F, Belliveau JF, Perron H;  
 XX  
 DR WPI; 1999-156177/14.  
 XX  
 PT Use of polypeptide derived from TRAIL protein for diagnosis of  
 PT degenerative disease - autoimmunity and inflammation, also useful in  
 PT prevention or treatment, and similar use of corresponding ligand and  
 PT nucleic acid.  
 XX

PS Claim 1; Page 13; 21pp; French.

CC The specification describes the use a polypeptide corresponding to at  
 CC least the primary sequence of part of the present sequence to produce a  
 CC diagnostic, prophylactic or therapeutic composition useful in cases of  
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can  
 CC be used in treatment of neurodegenerative diseases, lupus erythematosus,  
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central  
 CC nervous system cells, antigenic and specifically recognise the surface  
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and  
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an  
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific  
 CC receptors, inhibiting formation of natural complex  
 XX  
 SQ Sequence 281 AA;

Query Match 86.8%; Score 244; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-230;  
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTYYFTNELKQMDKYSKSGIACFLKE 60  
 QY 61 DSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120  
 DB 61 DSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQNIPLVRRGPQ 120  
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
 QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYPPDPILLMKSARNCSWKDAEYGLY 240  
 DB 181 FYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYPPDPILLMKSARNCSWKDAEYGLY 240  
 QY 241 SIYQ 244  
 DB 241 SIYQ 244

RESULT 65  
 AA01516  
 ID AA01516 standard; protein; 266 AA.  
 AC AA01516;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 13-JUN-2001 (first entry)

XX OmpA signal peptide-human TRAIL fusion protein.  
 DE  
 XX Human; attenuated tumour-targeted bacteria; effector molecule;  
 KW tumour necrosis factor; TNF; anti-angiogenic factor;  
 KW cytotoxic polypeptide; tumour inhibitory enzyme; therapy; carcinoma;  
 KW melanoma; lymphoma; sarcoma; metastasis; cytostatic; fusion protein;  
 KW TNF-alpha-related apoptosis-inducing ligand; TRAIL.  
 XX  
 OS Homo sapiens.  
 OS Escherichia coli.  
 OS Chimeric.  
 FH Key Location/Qualifiers  
 FT Peptide 1..21 /label= OmpA\_signal\_peptide  
 FT Region 23..266 /note= "Mature human TNF-alpha-related apoptosis-inducing  
 FT ligand"  
 XX  
 PN WO200125397-A2.  
 XX  
 PD 12-APR-2001.  
 XX

PF 24-AUG-2000; 2000WO-US023242.  
XX  
PR 04-OCT-1999; 99US-0157500P.  
PR 04-OCT-1999; 99US-0157581P.  
PR 04-OCT-1999; 99US-0157637P.  
XX  
PA (VION-) VION PHARM INC.  
XX  
XX Bermudes DG, King IC, Clairmont CA, Lin SL, Belcourt M;  
XX  
XX WPI; 2001-245063/25.  
DR N-PSDB; AAD03112.  
XX  
PT Attenuated tumor-targeted bacteria comprising nucleic acids encoding  
PT primary and secondary effector molecules, useful for the treatment of  
PT e.g. carcinomas, melanomas, lymphomas and sarcomas.  
XX  
PS Example 7; Fig 6; 185pp; English.  
XX  
CC The present invention relates to the preparation and use of attenuated  
CC tumour-targeted bacteria, such as, e.g., Salmonella, as a vector for the  
CC delivery of one or more primary effector molecules and secondary effector  
CC molecules to the site of a solid tumour. The primary effector molecules  
CC of the invention include members of the tumour necrosis factor (TNF),  
CC anti-angiogenic factors, cytotoxic polypeptides and tumour inhibitory  
CC enzymes. They induce a local immune response at the site of the tumour  
CC that results in the inhibition of growth of a tumour or tumour cells. The  
CC primary effector molecules are used for the treatment of solid tumours  
CC such as carcinomas, melanomas, lymphomas, sarcomas or metastases derived  
CC from these tumours. The present sequence is OmpA signal peptide-mature  
CC human TNF-alpha-related apoptosis-inducing ligand (TRAIL) fusion protein.  
CC The fusion of OmpA signal peptide to the amino terminus of TRAIL effector  
CC molecule enhances the periplasmic localisation and subsequent processing  
CC of the effector molecule. (Updated on 11-SEP-2003 to standardise OS  
CC field)  
XX  
SQ Sequence 266 AA;  
  
Query Match 86.1%; Score 242; DB 4; Length 266;  
Best Local Similarity 100.0%; Pred. No. 4e-228;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 40 NELKQMDKYSGKGIACFLKEDDSYDNDPDESMNSPCQVKWQLRQLVRKMLRTSSET 99  
DB 25 NELKQMDKYSGKGIACFLKEDDSYDNDPDESMNSPCQVKWQLRQLVRKMLRTSSET 84  
  
QY 100 ISTVQEKQNTISPLVRERGPQVAAHITGTRGRSNTLSPNSKNKALGRKINSWESSRS 159  
DB 85 ISTVQEKQNTISPLVRERGPQVAAHITGTRGRSNTLSPNSKNKALGRKINSWESSRS 144  
  
QY 160 GHSFLSNLHRLNGELVIEHKGFIYYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDDP 219  
DB 145 GHSFLSNLHRLNGELVIEHKGFIYYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDDP 204  
  
QY 220 ILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPL 279  
DB 205 ILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPL 264  
  
QY 280 VG 281  
DB 265 VG 266  
  
RESULT 66  
ADB61491  
ID ADB61491 standard; protein; 281 AA.  
XX  
AC ADB61491;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human Apo-2 ligand protein mutant D234C.  
XX

KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;  
KW high solvent accessibility; cytotostatic; antiarthritic; neuroprotective;  
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;  
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;  
KW human; mutant; mutein.  
XX  
OS Synthetic.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc-difference 234 /note= "Native residue of Asp is substituted by Cys"  
FT WO2003029420-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 01-OCT-2002; 2002WO-US031210.  
XX  
PR 02-OCT-2001; 2001US-0326622P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Kelley RF, Lindstrom SH;  
XX  
XX WPI; 2003-541400/51.  
XX  
Novel isolated Apo-2 ligand variant polypeptide useful for treating  
cancer or an immune-related disease such as multiple sclerosis, comprises  
amino acid substitutions in the native sequence of the Apo-2 ligand.  
  
Claim 1; Page; 92pp; English.  
  
The invention relates to a novel isolated Apo-2 ligand variant  
polypeptide having a sequence that differs from the native sequence  
having 281 amino acids given in specification. The Apo-2 ligand variant  
polypeptide is selected from a polypeptide having substitutions at  
residue positions identified from x-ray crystal structure of the  
DR5.Apo2L complex. The polypeptide having the substitutions made at  
residue position(s) selected from 20 positions such as S96C, S101C,  
S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,  
R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the  
residue position is, outside of the receptor contact region of the  
DR5.Apo2L complex, and displays high solvent accessibility in the crystal  
structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide  
and further compositions have the following activities: cytostatic,  
antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,  
an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for  
inducing apoptosis in mammalian cells, by exposing mammalian cells  
expressing a receptor selected from DR4 receptor and DR5 receptor to a  
therapeutically effective amount of the Apo-2 ligand variant polypeptide,  
Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are  
colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,  
the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for  
treating cancer (such as lung, breast, colon or colorectal cancer) or an  
immune-related disease (such as arthritis or multiple sclerosis) in a  
mammal, by administering to the mammal an effective amount of the Apo-2  
ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand  
trimer. This sequence represents the human Apo-2 ligand mutant D234C  
protein of the invention. NOTE: This sequence is not shown in the  
specification. It has been created from information provided in claim 1  
and from the sequence in Fig 1 of the specification.  
  
SQ Sequence 281 AA;  
  
Query Match 82.9%; Score 233; DB 7; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.7e-219;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYSGIACFLKE 60

```
QY 61 DSYWDPNDEESMNSPCQVKQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DSYWDPNDEESMNSPCQVKQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
QY 181 FYYIYSQTYFRQEEIKENTKNDKQKVQIYKYTSYDPDPILLMKSARNCSWK 233
DB 181 FYYIYSQTYFRQEEIKENTKNDKQKVQIYKYTSYDPDPILLMKSARNCSWK 233

RESULT 67
AAY27017
ID AAY27017 standard; protein; 281 AA.
XX
AC AAY27017;
XX
DT 24-SEP-1999 (first entry)
DE Human Apo-2 ligand (Apo-2L) variant D218A.
KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
KW lupus; immune-mediated glomerular nephritis; human; variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 218 /label= D218A
FT /note= "wild-type Asp is replaced with Ala"
XX
XX WO9936535-A1.
XX
XX 22-JUL-1999.
XX
XX 15-JAN-1999; 99WO-US001039.
XX
XX 15-JAN-1998; 98US-00007886.
XX 15-APR-1998; 98US-00060533.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
XX
XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
XX in mammalian cancer cells.
XX
XX Claim 10; Page; 86pp; English.
XX
XX The invention relates to a novel human cytokine, designated Apo-2 ligand
XX (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
XX methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
XX cells. This is useful for the treatment of cancer. Apo-2L can be used to
XX induce apoptosis for pathological conditions characterized by decreased
XX levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
XX mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
XX coding sequence can also be used in quantitative and screening diagnostic
XX techniques. Anti-Apo-2L antibodies can be used for treating diseases
XX associated with increased apoptosis. Sequences AAY27016-19 represent
XX specific examples of Apo-2L variants. Note: This sequence is not provided
XX in the specification. It has been created by modifying the wild-type Apo-
XX 2L sequence provided in Fig 1A
XX
XX Sequence 281 AA;
```

Query Match 77.2%; Score 217; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1.2e-203;  
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVATTVYFTNFKQMDKYSGKIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVATTVYFTNFKQMDKYSGKIACFLKE 60
QY 61 DSYWDPNDEESMNSPCQVKQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DSYWDPNDEESMNSPCQVKQKQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
QY 181 FYYIYSQTYFRQEEIKENTKNDKQKVQIYKYTSYP 217
DB 181 FYYIYSQTYFRQEEIKENTKNDKQKVQIYKYTSYP 217

RESULT 68
AAY27019
ID AAY27019 standard; protein; 281 AA.
XX
AC AAY27019;
XX
DT 24-SEP-1999 (first entry)
DE Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.
KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
KW lupus; immune-mediated glomerular nephritis; human; variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 203 /label= D203A
FT /note= "wild-type Asp is replaced with Ala"
FT Misc-difference 218 /label= D218A
FT /note= "wild-type Asp is replaced with Ala"
FT Misc-difference 269 /label= D269A
FT /note= "wild-type Asp is replaced with Ala"
XX
XX WO9936535-A1.
XX
XX 22-JUL-1999.
XX
XX 15-JAN-1999; 99WO-US001039.
XX
XX 15-JAN-1998; 98US-00007886.
XX 15-APR-1998; 98US-00060533.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
XX
XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
XX in mammalian cancer cells.
XX
XX Claim 12; Page; 86pp; English.
XX
XX The invention relates to a novel human cytokine, designated Apo-2 ligand
XX (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
XX methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
XX cells. This is useful for the treatment of cancer. Apo-2L can be used to
XX induce apoptosis for pathological conditions characterized by decreased
XX levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
XX mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
XX coding sequence can also be used in quantitative and screening diagnostic
```

CC techniques. Anti-Apo-2L antibodies can be used for treating diseases  
CC associated with increased apoptosis. Sequences AAY27016-19 represent  
CC specific examples of Apo-2L variants. Note: This sequence is not provided  
CC in the specification. It has been created by modifying the wild-type Apo-  
CC 2L sequence provided in Fig 1A

XX  
SQ Sequence 281 AA;  
Query Match 71.9%; Score 202; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 5.8e-189; Indels 0; Gaps 0;  
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCQVKQQLRQLVRKMLRTSEETISTVQSKQONISPLVRERGPO 120  
DB 61 DDSYWDPNDEESMNSPCQVKQQLRQLVRKMLRTSEETISTVQSKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
QY 181 FYIYSQTYFRFQBEIKENTKN 202  
DB 181 FYIYSQTYFRFQBEIKENTKN 202

RESULT 69  
AAY27016  
ID AAY27016 standard; protein; 281 AA.  
AC AAY27016;  
XX  
DT 24-SEP-1999 (first entry)  
DE Human Apo-2 ligand (Apo-2L) variant D203A.  
KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;  
KW lupus; immune-mediated glomerular nephritis; human; variant.  
XX  
OS Homo sapiens.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Misc-difference 203 /label= D203A  
FT /note= "wild-type Asp is replaced with Ala"

XX WO936535-A1.  
XX  
PD 22-JUL-1999.  
XX  
XX 15-JAN-1999; 99WO-US001039.  
XX PF  
XX 15-JAN-1998; 98US-00007886.  
XX PR  
XX 15-APR-1998; 98US-00060533.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;  
XX WPI; 1999-444397/37.  
XX  
XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis  
XX in mammalian cancer cells.  
XX  
XX Claim 9; Page; 86pp; English.  
XX  
XX The invention relates to a novel human cytokine, designated Apo-2 ligand  
XX (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant  
XX methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer

CC cells. This is useful for the treatment of cancer. Apo-2L can be used to  
CC induce apoptosis for pathological conditions characterized by decreased  
CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-  
CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid  
CC coding sequence can also be used in quantitative and screening diagnostic  
CC techniques. Anti-Apo-2L antibodies can be used for treating diseases  
CC associated with increased apoptosis. Sequences AAY27016-19 represent  
CC specific examples of Apo-2L variants. Note: This sequence is not provided  
CC in the specification. It has been created by modifying the wild-type Apo-  
CC 2L sequence provided in Fig 1A

XX  
SQ Sequence 281 AA;  
Query Match 71.9%; Score 202; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 5.8e-189; Indels 0; Gaps 0;  
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLQMDKYSGGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCQVKQQLRQLVRKMLRTSEETISTVQSKQONISPLVRERGPO 120  
DB 61 DDSYWDPNDEESMNSPCQVKQQLRQLVRKMLRTSEETISTVQSKQONISPLVRERGPO 120  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
QY 181 FYIYSQTYFRFQBEIKENTKN 202  
DB 181 FYIYSQTYFRFQBEIKENTKN 202

RESULT 70  
ABG72257  
ID ABG72257 standard; protein; 281 AA.  
XX  
AC ABG72257;  
XX  
DT 04-MAR-2003 (first entry)  
DE Human tumour related apoptosis inducing ligand (Trail).  
XX  
XX Human; tumour related apoptosis inducing ligand; Trail;  
KW Trail prokaryotic expression system; tumour cell death.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 217 /note= "Encoded by CTT"  
FT  
FT  
XX CN1354183-A.  
XX  
XX 19-JUN-2002.  
XX  
XX 30-NOV-2001; 2001CN-00132371.  
XX PF  
XX 30-NOV-2001; 2001CN-00132371.  
XX PR  
XX (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.  
XX PA  
XX Hu Y, Yao Y;  
XX  
XX WPI; 2002-751439/82.  
XX DR  
XX N-PSDB; ABX14391.  
XX  
XX Tumour death induction ligand gene, gene expression protein and its  
XX preparation method.  
XX  
XX Claim 7; Page 10 (disclosure); 17pp; Chinese.  
XX

CC The present invention relates to the isolation of cDNA encoding human  
 CC tumour related apoptosis inducing ligand (TRAIL), and the TRAIL protein.  
 CC The TRAIL full length cDNA is cloned, and is utilised to create a TRAIL  
 CC prokaryotic expression system. The full length TRAIL cDNA is used to  
 CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail  
 CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic  
 CC expression systems. The prokaryotic expression systems created greatly  
 CC increase the expression and quantity of the Trail, Trail109, and Trail114  
 CC proteins, and may be useful in a new preparation for killing tumour  
 CC cells. The present sequence represents the full length human Trail  
 CC protein  
 XX  
 XX  
 XX Sequence 281 AA;

Query Match 70.8%; Score 199; DB 5; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 5e-186;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60  
 QY 61 DSDYNDPNDDESNMSPCWQVKQLRQLVKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 DB 61 DSDYNDPNDDESNMSPCWQVKQLRQLVKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
 QY 181 FYIYSQTYFRFQEEIKEN 199  
 DB 181 FYIYSQTYFRFQEEIKEN 199

## RESULT 71

AAU99301 ID AAU99301 standard; protein; 212 AA.

XX AC AAU99301;  
 XX  
 XX 24-SEP-2002 (first entry)  
 XX Human TRAIL splice variant 8, rpl-6-6, protein.  
 XX Human; cytostatic; neuroprotective; immunosuppressive; splice variant;  
 KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;  
 KW TRAIL; apoptosis; programmed cell death; differentiation; development;  
 KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;  
 KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;  
 KW therapeutic; neurodegenerative disease; autoimmune disease; aging;  
 KW chromosome 3q26; rpl-6-6.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Domain 1..16  
 FT /note= "Cytoplasmic domain"  
 FT Domain 17..38  
 FT /note= "Transmembrane domain"  
 FT Domain 39..212  
 FT /note= "Extracellular domain"  
 FT Misc-difference 209  
 FT /note= "Encoded by in-frame stop codon"  
 XX  
 XX US2002061525-A1.  
 XX  
 XX 23-MAY-2002.  
 XX  
 XX 16-MAY-2001; 2001US-00855544.  
 XX  
 XX 16-MAY-2000; 2000IL-00136156.  
 XX

PA (YELI/) YELIN R.  
 PA (KHOS/) KHOSRAVI R.  
 PA (SAVI/) SAVITZKY R.  
 XX  
 XX Yelin R, Khosravi R, Savitzky K;  
 XX WPI; 2002-479259/51.  
 XX  
 XX New splice variants of tumor necrosis factor-related apoptosis inducing  
 PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat  
 PT diseases or disorders associated with low expression of the variants.  
 XX  
 XX Claim 4; Fig 8; 29pp; English.

CC The invention discloses isolated, naturally occurring, polypeptide splice  
 CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing  
 CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal  
 CC cellular differentiation and development of multicellular organisms.  
 CC Apoptosis is induced by certain cytokines which include TNF and TRAIL  
 CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane  
 CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in  
 CC many tissues and cells. Receptors for TRAIL include two death domain  
 CC containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1  
 CC and DcR2, lacking the intracellular signalling death domain. TRAIL,  
 CC induced by type I interferons, induces apoptosis in tumour cells, whereas  
 CC normal cells are relatively resistant without showing significant toxic  
 CC side effects. Thus, TRAIL has the potential to be a very useful  
 CC antitumour agent. The naturally occurring splice variants may differ in  
 CC their cellular distribution, expression levels/timing and activity.  
 CC Determining these factors could provide possible mechanisms for the  
 CC induction of apoptosis of tumour cells. The splice variant polypeptides  
 CC and polynucleotides can be used in gene therapy, to raise antibodies, to  
 CC detect the levels, distribution and ratios of expression of TRAIL, and  
 CC its splice variants, in a biological sample and to identify compounds  
 CC which bind the variant TRAIL products and modulate its activity (agonists  
 CC and antagonists). Pharmaceutical compositions, comprising an expression  
 CC vector or any of the amino acid sequences, are useful for causing a  
 CC cytotoxic effect in cancer cells and for treatment of diseases which can  
 CC be ameliorated, cured or prevented by lowering or raising the level of  
 CC the amino acid sequences. The antibodies may also have a therapeutic  
 CC utility in blocking or decreasing the activity of the TRAIL variant  
 CC products. Diseases that may be treated include cancer, neurodegenerative  
 CC diseases, autoimmune diseases, diseases involved in the non-normal  
 CC development of tissues and aging. TRAIL's gene is located on chromosome  
 CC 3q26. The sequence presented is the human TNF-related apoptosis inducing  
 CC ligand (TRAIL) splice variant 8, rpl-6-6, protein which has had an C-  
 CC terminal section of the conserved TNF domain deleted

XX Sequence 212 AA;

Query Match 68.7%; Score 193; DB 5; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 3e-180;  
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60  
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60  
 QY 61 DSDYNDPNDDESNMSPCWQVKQLRQLVKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 DB 61 DSDYNDPNDDESNMSPCWQVKQLRQLVKMLRTSEETISTVQEKQNIPLVRERGQ 120  
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180  
 QY 181 FYIYSQTYFRFQ 193  
 DB 181 FYIYSQTYFRFQ 193

RESULT 72  
 ADK72306

ID ADK72306 standard; protein; 281 AA.  
AC ADK72306;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human Apo-2 ligand variant #2.  
XX  
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
KW human; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 189 /note= "wild-type Tyr replaced by Ala"  
FT Misc-difference 191 /note= "wild-type Arg replaced by Lys"  
FT Misc-difference 193 /note= "wild-type Gln replaced by Lys"  
FT Misc-difference 264 /note= "wild-type His replaced by Ala"  
FT  
XX  
PN WO2004001009-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 23-JUN-2003; 2003WO-US019750.  
XX  
PR 24-JUN-2002; 2002US-0391050P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Hymowitz S, Kelley RF, Lindstrom SH;  
XX  
DR WPI; 2004-082490/08.  
XX  
PT New Apo-2 ligand variant polypeptide, useful for preparing a composition  
PT for treating cancer or immune-related disease, e.g., arthritis or  
PT multiple sclerosis.  
XX  
PS Claim 9; Page; 111pp; English.  
XX  
CC The invention relates to a novel isolated Apo-2 ligand variant  
CC polypeptide, comprising a sequence that differs from the native sequence  
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having  
CC one or more following amino acid substitutions at the residue positions  
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an  
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand  
CC variant polypeptide. Further disclosed are a composition comprising the  
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a  
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant  
CC polypeptide is useful for preparing a composition for treating cancer or  
CC immune-related disease, e.g., arthritis or multiple sclerosis. The  
CC current sequence represents a human Apo-2 ligand mutant. Note: This  
CC sequence is not found in the specification, but may be created using the  
CC wild-type Apo-2 ligand sequence given in ADK72296.  
XX  
SQ Sequence 281 AA;  
Query Match 66.9%; Score 188; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-175;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVATYVYFTNELKQMDKYKSGIACFLKE 60  
DB 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVATYVYFTNELKQMDKYKSGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCWQKVKQLRQLVKRMILR7SEETISTVQSKQNIPLVRERGQ 120  
DB 61 DDSYWDPNDEESMNSPCWQKVKQLRQLVKRMILR7SEETISTVQSKQNIPLVRERGQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
QY 181 FYIYSQT 188  
DB 181 FYIYSQT 188  
RESULT 73  
ADK72313  
ID ADK72313 standard; protein; 281 AA.  
XX  
AC ADK72313;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human Apo-2 ligand variant #7.  
XX  
KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
KW human; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 189 /note= "wild-type Tyr replaced by Gln"  
FT Misc-difference 191 /note= "wild-type Arg replaced by Lys"  
FT Misc-difference 193 /note= "wild-type Gln replaced by Arg"  
FT Misc-difference 266 /note= "wild-type Ile replaced by Leu"  
FT  
XX  
PN WO2004001009-A2.  
XX  
PD 31-DEC-2003.  
XX  
PF 23-JUN-2003; 2003WO-US019750.  
XX  
PR 24-JUN-2002; 2002US-0391050P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Hymowitz S, Kelley RF, Lindstrom SH;  
XX  
DR WPI; 2004-082490/08.  
XX  
PT New Apo-2 ligand variant polypeptide, useful for preparing a composition  
PT for treating cancer or immune-related disease, e.g., arthritis or  
PT multiple sclerosis.  
XX  
PS Claim 22; Page; 111pp; English.  
XX  
CC The invention relates to a novel isolated Apo-2 ligand variant  
CC polypeptide, comprising a sequence that differs from the native sequence  
CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having  
CC one or more following amino acid substitutions at the residue positions  
CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an  
CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand  
CC variant polypeptide. Further disclosed are a composition comprising the  
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a  
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant  
CC polypeptide is useful for preparing a composition for treating cancer or  
CC immune-related disease, e.g., arthritis or multiple sclerosis. The  
CC current sequence represents a human Apo-2 ligand mutant. Note: This  
CC sequence is not found in the specification, but may be created using the  
CC wild-type Apo-2 ligand sequence given in ADK72296.  
XX  
SQ Sequence 281 AA;

Query Match 66.9%; Score 188; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-175;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLKQMDKYSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120  
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQT 188  
DB 181 FYIYSQT 188

RESULT 74  
ADK72305  
ID ADK72305 standard; protein; 281 AA.  
XX AC ADK72305;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human Apo-2 ligand variant #1.  
XX KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
XX KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
XX KW human; mutein.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Misc-difference 189 /note= "wild-type Tyr replaced by Ala"  
FT Misc-difference 191 /note= "wild-type Arg replaced by Lys"  
FT Misc-difference 193 /note= "wild-type Gln replaced by Lys"  
XX PN WO2004001009-A2.  
XX PD 31-DEC-2003.  
XX PF 23-JUN-2003; 2003WO-US019750.  
XX PR 24-JUN-2002; 2002US-0391050P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Hymowitz S, Kelley RF, Lindstrom SH;  
XX DR WPI; 2004-082490/08.  
XX FT New Apo-2 ligand variant polypeptide, useful for preparing a composition  
XX FT for treating cancer or immune-related disease, e.g., arthritis or  
XX FT multiple sclerosis.  
XX PS Claim 9; Page; 11pp; English.  
XX CC The invention relates to a novel isolated Apo-2 ligand variant  
XX CC polypeptide, comprising a sequence that differs from the native sequence  
XX CC Apo-2 ligand polypeptide sequence comprising 282 amino acids and having  
XX CC one or more following amino acid substitutions at the residue positions  
XX CC comprising S96C, S101C, S111C, R170C or K179C. Also disclosed is an  
XX CC isolated nucleic acid molecule comprising DNA encoding the Apo-2 ligand

CC variant polypeptide. Further disclosed are a composition comprising the  
CC Apo-2 ligand variant polypeptide, a method of treating cancer, and a  
CC method of inducing apoptosis in mammalian cells. The Apo-2 ligand variant  
CC polypeptide is useful for preparing a composition for treating cancer or  
CC immune-related disease, e.g., arthritis or multiple sclerosis. The  
CC current sequence represents a human Apo-2 ligand mutant. Note: This  
CC sequence is not found in the specification, but may be created using the  
CC wild-type Apo-2 ligand sequence given in ADK72296.  
XX SQ Sequence 281 AA;

Query Match 66.9%; Score 188; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.9e-175;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLKQMDKYSGIACFLKE 60  
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNKLKQMDKYSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120  
DB 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQT 188  
DB 181 FYIYSQT 188

RESULT 75  
ADK72309  
ID ADK72309 standard; protein; 281 AA.  
XX AC ADK72309;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human Apo-2 ligand variant #5.  
XX KW Cytostatic; antiarthritic; neuroprotective; gene therapy; Apo-2 ligand;  
XX KW variant; cancer; immune system disease; arthritis; multiple sclerosis;  
XX KW human; mutein.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Misc-difference 189 /note= "wild-type Tyr replaced by Ala"  
FT Misc-difference 191 /note= "wild-type Arg replaced by Lys"  
FT Misc-difference 193 /note= "wild-type Gln replaced by Arg"  
FT Misc-difference 264 /note= "wild-type His replaced by Ser"  
FT Misc-difference 266 /note= "wild-type Ile replaced by Leu"  
FT Misc-difference 269 /note= "wild-type Asp replaced by Glu"  
XX PN WO2004001009-A2.  
XX PD 31-DEC-2003.  
XX PF 23-JUN-2003; 2003WO-US019750.  
XX PR 24-JUN-2002; 2002US-0391050P.  
XX PA (GETH ) GENENTECH INC.  
XX XX



Search completed: June 22, 2005, 06:48:54  
Job time : 172 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2005, 06:52:03 ; Search time 161 Seconds  
(without alignments)  
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Title: US-10-662-429-2

Perfect score: 281

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Scoring table:

Gapop 60.0 , Capext 60.0

Searched: 1714042 seqs, 383979560 residues

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Post-processing: Listing first 100 summaries

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- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	100.0	281	8	US-08-916-6259-6
2	281	100.0	281	8	US-08-971-317A-8
3	281	100.0	281	9	US-09-813-329-17
4	281	100.0	281	9	US-09-193-663-8
5	281	100.0	281	9	US-09-334-465-1
6	281	100.0	281	10	US-09-919-039-118
7	281	100.0	281	13	US-10-011-125-4
8	281	100.0	281	13	US-10-001-054-54
9	281	100.0	281	14	US-10-093-766-54
10	281	100.0	281	14	US-10-174-654-11
11	281	100.0	281	14	US-10-151-882-41
12	281	100.0	281	14	US-10-151-882-41
13	281	100.0	281	14	US-10-151-882-41
14	281	100.0	281	14	US-10-151-882-41
15	281	100.0	281	14	US-10-151-882-41
16	281	100.0	281	14	US-10-151-882-41
17	281	100.0	281	14	US-10-151-882-41
18	281	100.0	281	14	US-10-151-882-41
19	281	100.0	281	14	US-10-151-882-41
20	281	100.0	281	14	US-10-151-882-41
21	281	100.0	281	14	US-10-151-882-41
22	281	100.0	281	14	US-10-151-882-41
23	281	100.0	281	14	US-10-151-882-41
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81	281	100.0	281	14	US-10-151-882-41
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84	281	100.0	281	14	US-10-151-882-41

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Sequence 31, Appl  
Sequence 9, Appl  
Sequence 12, Appl  
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Sequence 20, Appl  
Sequence 33427, A  
Sequence 11, Appl  
Sequence 12, Appl

85 34 12.1 34 14 US-10-272-411-24 Sequence 24, Appl  
86 34 12.1 34 14 US-10-272-328A-24 Sequence 24, Appl  
87 15 5.3 15 17 US-10-625-073-14 Sequence 14, Appl  
88 15 5.3 19 17 US-10-625-073-32 Sequence 32, Appl  
89 14 5.0 172 9 US-09-773-050A-17 Sequence 17, Appl  
90 14 5.0 287 16 US-10-367-094-15 Sequence 15, Appl  
91 14 5.0 291 10 US-09-873-829-6 Sequence 6, Appl  
92 14 5.0 291 13 US-10-017-910-6 Sequence 6, Appl  
93 14 5.0 291 15 US-10-652-244-6 Sequence 6, Appl  
94 12 4.3 87 14 US-10-286-696-13 Sequence 13, Appl  
95 12 4.3 87 16 US-10-890-368-13 Sequence 13, Appl  
96 12 4.3 87 16 US-10-889-948-13 Sequence 13, Appl  
97 11 3.9 21 15 US-10-399-018-21 Sequence 21, Appl  
98 10 3.6 10 14 US-10-272-411-25 Sequence 25, Appl  
99 10 3.6 10 14 US-10-272-328A-25 Sequence 25, Appl  
100 9 3.2 9 14 US-10-272-411-27 Sequence 27, Appl

ALIGNMENTS

RESULT 1  
US-08-916-625B-6  
; Sequence 6, Application US/08916625B  
; Publication No. US20010010924A1  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH C.  
; APPLICANT: YOUNG, PETER R.  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED  
; TITLE OF INVENTION: RECEPTOR, TR6  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-SEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/916,625B  
; FILING DATE: 22-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/853,684  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: 60/041,230  
; FILING DATE: 14-MARCH-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-50008-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-916-625B-6  
Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNKLQKMODKYSKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNKLQKMODKYSKSGIACFLKE 60  
QY 61 DSDVWDPNDESMSPCQVQWQLRQLVRKWLRTSEETISTVQEKQONISPLVREGRGPQ 120  
Db 61 DSDVWDPNDESMSPCQVQWQLRQLVRKWLRTSEETISTVQEKQONISPLVREGRGPQ 120  
QY 121 RVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Db 121 RVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
QY 181 FYYISQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240  
Db 181 FYYISQTYFRQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSAARNCSWSDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281  
Db 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281  
RESULT 2  
US-08-971-317A-8  
; Sequence 8, Application US/08971317A  
; Publication No. US20010010925A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: Fast-SEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/971,317A  
; FILING DATE: 17-NOV-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goller, Mimi C  
; REGISTRATION NUMBER: 39,046  
; REFERENCE/DOCKET NUMBER: 6255.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (847) 935-7550  
; TELEFAX: (847) 938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. US20010010925A1  
US-08-971-317A-8  
Query Match 100.0%; Score 281; DB 8; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNKLQKMODKYSKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVVYFTNKLQKMODKYSKSGIACFLKE 60

61	Qy	DDSYNDPNDEESMNSPCQVQWKQLRQLVRKMLIRLTSSEETISTVQEKQKQINISPLVRERGQ	120
61	Db	DDSYNDPNDEESMNSPCQVQWKQLRQLVRKMLIRLTSSEETISTVQEKQKQINISPLVRERGQ	120
121	Qy	RVAAHITCTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHKG	180
121	Db	RVAAHITCTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHKG	180
181	Qy	FYYIYSQTYFQFEIKENTKNDKQMVQYIYKYTSYPDPILLMKASRNSCWKDABEYGL	240
181	Db	FYYIYSQTYFQFEIKENTKNDKQMVQYIYKYTSYPDPILLMKASRNSCWKDABEYGL	240
241	Qy	SIYGGIFELKENDRIFSVYVTHNEHLIDMDHEASFFGAFVIG	281
241	Db	SIYGGIFELKENDRIFSVYVTHNEHLIDMDHEASFFGAFVIG	281

### RESULT 3

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US-09-813-329-17
;
; Sequence 17, Application US/09813329
; Patent No. US2002012968A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Bristol-Myers Squibb Company
;
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Molecule
;
; TITLE OF INVENTION: Variants thereof
;
; FILE REFERENCE: D0016.jp
;
; CURRENT APPLICATION NUMBER: US/09/813,329
;
; CURRENT FILING DATE: 2001-03-20
;
; PRIOR APPLICATION NUMBER: 60/190,816
;
; PRIOR FILING DATE: 2000-03-21
;
; NUMBER OF SEQ ID NOS: 65
;
; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 17
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; LENGTH: 281
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; TYPE: PRT
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; ORGANISM: Drosophila melanogaster
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; US-09-813-329-17

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Query Match	100.0%	Score 281;	DB 9;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 6.4e-272;		
Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	MAMMEVGGPSLG	QTCVLIIVFTVLLQSLCAVATVYVFTNELKQMDKYSKSGIACFLKE	60
Qy	61	DDSYMDNDEESMNS	PCQVKWQRLQRLVKRMILRTSEETISTVQEKQONISPLVRERGPQ	120
Db	61	DDSYMDNDEESMNS	PCQVKWQRLQRLVKRMILRTSEETISTVQEKQONISPLVRERGPQ	120
Qy	121	RVAAHITGTRGRSNTL	SPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVVIHEKG	180
Db	121	RVAAHITGTRGRSNTL	SPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVVIHEKG	180
Qy	181	FYYIYSQTYFRFQEEI	KENTKNDQMQVYIYKYTSYDPDPIILLMKSARNCSWKDAEYGLY	240
Db	181	FYYIYSQTYFRFQEEI	KENTKNDQMQVYIYKYTSYDPDPIILLMKSARNCSWKDAEYGLY	240
Qy	241	SIYGGGIFELKENDRI	IFVSVTNEHLIDMDHEASFFGAPLVG	281
Db	241	SIYGGGIFELKENDRI	IFVSVTNEHLIDMDHEASFFGAPLVG	281

## RESULT 4

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US-09-193-663-8
RESD001 4
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION NUMBER: US/09/193.663

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; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8

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Query Match	100.0%;	Score 281;	DB 9;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 6.4e-272;		
Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MANMEVGGPSLGQTCVLIVIFVTLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE	60	
Db	1	MANMEVGGPSLGQTCVLIVIFVTLLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE	60	
Qy	61	DDSYWPDNDBEESMNSPCQWKQMLROLRVKMIILRTSEETISTVQEKQOONISPLVRBRGPQ	120	
Db	61	DDSYWPDNDBEESMNSPCQWKQMLROLRVKMIILRTSEETISTVQEKQOONISPLVRBRGPQ	120	
Qy	121	RVAAHITGTRGRNTLISSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRANGELVVIHEKG	180	
Db	121	RVAAHITGTRGRNTLISSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRANGELVVIHEKG	180	
Qy	181	FYIYISQTYFRFOEIKENTKNDKQMVQIYKYTYSYDPDILLMKSARNSCWSKDAEYGLY	240	
Db	181	FYIYISQTYFRFOEIKENTKNDKQMVQIYKYTYSYDPDILLMKSARNSCWSKDAEYGLY	240	
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG	281	
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG	281	

## RESULT 5

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US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

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	Query Match	100.0%;	Score 281;	DB 9;	Length 281;
	Best Local Similarity	100.0%;	Pred. No. 6.4e-272;		
	Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MANMEVGGPSLGQTCLVIFVTLQSLQSLCAVTVYVFTNELQMDQDKYSKSGIACFLKE	60		
Db	1	MANMEVGGPSLGQTCLVIFVTLQSLQSLCAVTVYVFTNELQMDQDKYSKSGIACFLKE	60		
Qy	61	DDSYWDPNDBEESMNSPCWQVQKWQLRLVRKMIILRTSETISTVQEKQONISPLVRERGPQ	120		
Db	61	DDSYWDPNDBEESMNSPCWQVQKWQLRLVRKMIILRTSETISTVQEKQONISPLVRERGPQ	120		
Qy	121	RVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG	180		
Db	121	RVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVTHEKG	180		
Qy	181	FYIYISOTVFRFOEIKENTKNDKQWQVIYKYKTSYDPDPIILLMKSRNCSWSKDAEYGLY	240		

Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 6

US-09-919-039-118  
; Sequence 118, Application US/09919039  
; Publication No. US20030108871A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; FILE REFERENCE: PA-0035 US  
; CURRENT APPLICATION NUMBER: US/09/919,039  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/222,113  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 401  
; SOFTWARE: PERL Program  
; SEQ ID NO 118  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1  
US-09-919-039-118

Query Match 100.0%; Score 281; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272; Indels 0; Gaps 0;  
Matches 281; Conservative 0; Mismatches 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
QY 61 DDSYWDNDDESMNSPCQVQKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
Db 61 DDSYWDNDDESMNSPCQVQKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
QY 121 RVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Db 121 RVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
QY 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLY 240  
Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

US-10-011-125-4  
; Sequence 4, Application US/10011125  
; Publication No. US20020142388A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Christina Yu-Ching  
; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
; FILE REFERENCE: P1804R1  
; CURRENT APPLICATION NUMBER: US/10/011,125  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/256,162  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 4  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-011-125-4

Query Match 100.0%; Score 281; DB 13; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272; Indels 0; Gaps 0;  
Matches 281; Conservative 0; Mismatches 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
QY 61 DDSYWDNDDESMNSPCQVQKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
Db 61 DDSYWDNDDESMNSPCQVQKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPQ 120  
QY 121 RVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
Db 121 RVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180  
QY 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLY 240  
Db 181 FYYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

US-10-001-054-54  
; Sequence 54, Application US/10001054  
; Publication No. US20020192209A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Baker, Kevin  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hebert, Carolyn  
; APPLICANT: Henzel, William  
; APPLICANT: Kabakoff, Rhona  
; APPLICANT: Shelton, David  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
; FILE OF INVENTION: CELL GROWTH  
; FILE REFERENCE: P3034R1PCT  
; CURRENT APPLICATION NUMBER: US/10/001,054  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/082999  
; PRIOR FILING DATE: 1998-04-24  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/085149  
; PRIOR FILING DATE: 1998-05-12  
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; PRIOR FILING DATE: 1998-06-02  
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; PRIOR APPLICATION NUMBER: 60/096891  
; PRIOR FILING DATE: 1998-08-17  
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; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 60/099803  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100263

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; PRIOR FILING DATE: 1998-09-14  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
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; PRIOR APPLICATION NUMBER: 60/107783  
; PRIOR FILING DATE: 1998-11-10  
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; PRIOR FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 60/113296  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/115554  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115558  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/116533  
; PRIOR FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 60/123618  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: 60/131294  
; PRIOR FILING DATE: 1999-04-07  
; PRIOR APPLICATION NUMBER: 60/140650  
; PRIOR FILING DATE: 1999-06-22  
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; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/144758  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/162506  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 60/170262  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 60/187202  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/209832  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: 60/232887  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/180997  
; PRIOR FILING DATE: 1998-11-19  
; PRIOR APPLICATION NUMBER: 09/218517  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 09/284291  
; PRIOR FILING DATE: 1999-04-12  
; PRIOR APPLICATION NUMBER: 09/380137  
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; PRIOR APPLICATION NUMBER: 09/423741  
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; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 09/866034  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 09/872035  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: 09/882636  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 09/924419  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/927796  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/929404  
; PRIOR FILING DATE: 2001-08-13

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; PRIOR APPLICATION NUMBER: 09/941992  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 09/946374  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: PCT/US98/18824  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: PCT/US99/00106  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: PCT/US99/05028  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: PCT/US99/08615  
; PRIOR FILING DATE: 1999-04-20  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: PCT/US99/20111  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28634  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00376  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: PCT/US00/04341  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04342  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/06884  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/US00/13705  
; PRIOR FILING DATE: 2000-05-17  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: PCT/US00/14941  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/22031  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: PCT/US00/23522  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: PCT/US00/30873  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/06666  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: PCT/US01/17092  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/US01/21066  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: PCT/US01/27099

;; PRIOR FILING DATE: 2001-08-29  
;; NUMBER OF SEQ ID NOS: 91  
;; SEQ ID NO 54  
;; LENGTH: 281  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-001-054-54

Query Match 100.0%; Score 281; DB 13; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNKLQMDKYKSGIACFLKE 60  
DB 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNKLQMDKYKSGIACFLKE 60  
  
QY 61 DDSYNDPNDDESMNSPCQVKQKQLRQLVKMLRTSEETISTVQEQQNISPLVREGRGP 120  
DB 61 DDSYNDPNDDESMNSPCQVKQKQLRQLVKMLRTSEETISTVQEQQNISPLVREGRGP 120  
  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
  
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
  
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9

US-10-093-766-54  
; Sequence 54, Application US/10093766  
; Publication No. US20030013099A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy W.  
; APPLICANT: Jones, David A.  
; APPLICANT: Karpf, Adam R.  
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS  
; FILE REFERENCE: PA-0047 US  
; CURRENT APPLICATION NUMBER: US/10/093,766  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PERL Program  
; SEQ ID NO 54  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CDI  
US-10-093-766-54

Query Match 100.0%; Score 281; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNKLQMDKYKSGIACFLKE 60  
DB 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNKLQMDKYKSGIACFLKE 60  
  
QY 61 DDSYNDPNDDESMNSPCQVKQKQLRQLVKMLRTSEETISTVQEQQNISPLVREGRGP 120  
DB 61 DDSYNDPNDDESMNSPCQVKQKQLRQLVKMLRTSEETISTVQEQQNISPLVREGRGP 120  
  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
  
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240

DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
  
QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
DB 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
  
RESULT 10  
US-10-174-654-11  
; Sequence 11, Application US/10174654  
; Publication No. US20030044937A1  
; GENERAL INFORMATION:  
; APPLICANT: Bienkowski, Michael J  
; Mills, Cynthia J  
; Jones, David A  
; TITLE OF INVENTION: TNF-Related Death Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property  
; Legal Services  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/174,654  
; FILING DATE: 19-Jun-2002  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerber, Lori L.  
; REGISTRATION NUMBER: 41,113  
; REFERENCE/DOCKET NUMBER: 6111.N CN1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616/833-0974  
; TELEFAX: 616/833-8897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-174-654-11

Query Match 100.0%; Score 281; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNKLQMDKYKSGIACFLKE 60  
DB 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYYFTNKLQMDKYKSGIACFLKE 60  
  
QY 61 DDSYNDPNDDESMNSPCQVKQKQLRQLVKMLRTSEETISTVQEQQNISPLVREGRGP 120  
DB 61 DDSYNDPNDDESMNSPCQVKQKQLRQLVKMLRTSEETISTVQEQQNISPLVREGRGP 120  
  
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
  
QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
DB 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240



<b>Qy</b>	241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281 
<b>D<sub>b</sub></b>	241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281 

RESULT 11

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US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor
; FILE REFERENCE: PFS54
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-41

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Query Match	100.0%	Score 281;	DB 14;	Length 281;
Best Local Similarity	100.0%;	Pred. No. 6.4e-372;		
Matches ~281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAMMEVGGPSLGQTCVLII	FTVLLQSLCAVATVYVFTNELKQMDKYKSGIACFLKE	60
Db	1	MAMMEVGGPSLGQTCVLII	FTVLLQSLCAVATVYVFTNELKQMDKYKSGIACFLKE	60
Qy	61	DDSYWDNDSESMNSPCWQVKWQLRQLRVKMLLTSEET	ISTVQEKQONISPLVREGPQ	120
Db	61	DDSYWDNDSESMNSPCWQVKWQLRQLRVKMLLTSEET	ISTVQEKQONISPLVREGPQ	120
Qy	121	RVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHS	FUSNLHRLRNGELVIEHG	180
Db	121	RVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHS	FUSNLHRLRNGELVIEHG	180
Qy	181	FYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTTSYDPD	ILLMKMSARNCSWSDAEGLY	240
Db	181	FYIYSQTYFRFQBEIKENTKNDKQMVQIYKYTTSYDPD	ILLMKMSARNCSWSDAEGLY	240
Qy	241	SIYGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG		281
Db	241	SIYGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG		281

## RESULT 12

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US-10-218-547-20
; Sequence 20, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-218-547-20

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Query Match	100.0.0%;	Score 281;	DB 14;	Length 281;
Best Local Similarity	100.0.0%;	Pred. No. 6.4e-272;		
Matches 281; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAMMEVGGPSLQGTCLIVIFVTLLQSICVAITYYFTTNELKQMOKDKYSKSGIACFLKE	60	
Dd	1	MAMMEVGGPSPGQTCLIVIFVTLLQSICVAITYYFTTNELKQMOKDKYSKSGIACFLKE	60	
Qy	61	DDSYWDPNDEESNNSPCWQVKMQLRVLVRKMILLRTSEETISTVOEKQOINISPLVRRGPQ	120	
Dd	61	DDSYWDPNDEESNNSPCWQVKMQLRVLVRKMILLRTSEETISTVOEKQOINISPLVRRGPQ	120	
Qy	121	RVAAHITGRGRNTLSSPNSSKNEKALGRKINSWESSRGHSPLSNLHLRNGELVITHKG	180	
Dd	121	RVAAHITGRGRNTLSSPNSSKNEKALGRKINSWESSRGHSPLSNLHLRNGELVITHKG	180	
Qy	181	FYYIYSQTYPRFOEIKENTQDKMQVQIYKYTTSYPDPIILMKSAARNCSWKDAEYGly	240	
Dd	181	FYYIYSQTYPRFOEIKENTKNDKQMVQIYKYTTSYPDPIILMKSAARNCSWKDAEYGly	240	
Qy	241	SIYOGGIPELKENDRIFVSVTNEHLIDMDHEASFFCGAFLVG	281	
Dd	241	SIYOGGIPELKENDRIFVSVTNEHLIDMDHEASFFCGAFLVG	281	

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RESULT 13
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72

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	Query Match	100.0%;	Score 281;	DB 14;	Length 281;
	Best Local Similarity	100.0%;	Pred. No. 6.4e-272;		
	Matches 281;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAMMEVGGGSPSLGQT	CVLIVIFTVLLQSLCAVATYYVYFTNELKQMDKYKSGIACFLKE	60	
Db	1	MAMMEVGGGSPSLGQT	CVLIVIFTVLLQSLCAVATYYVYFTNELKQMDKYKSGIACFLKE	60	
Qy	61	DDSYWDPNDBEESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKQINISPLVREERGQ	120		
Db	61	DDSYWDPNDBEESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKQINISPLVREERGQ	120		
Qy	121	RVAAHITGTRGRSNTLUSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVTHEKG	180		
Db	121	RVAAHITGTRGRSNTLUSSPNSKNEKALGRKINSWESSRSCHSFLSNLHLRNGELVTHEKG	180		
Qy	181	FYYIYQTYFRFQEEIKENTQNDKQWQVQIYKYTSPYDPILLMKKSARNSCWSKDAEYGLY	240		

Db 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSGARNCSWKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14  
US-10-139-785-66  
; Sequence 66, Application US/10139785  
; Publication No. US20030190685A1  
; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
; FILE REFERENCE: PF550  
; CURRENT APPLICATION NUMBER: US/10/139,785  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 60/369,860  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/341,237  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/331,310  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/331,044  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/327,364  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: 60/323,807  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/309,176  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/294,981  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 60/293,473  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-139-785-66

Query Match 100.0%; Score 281; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272; Mismatches 0; Indels 0; Gaps 0;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60  
QY 61 DSYWDPNDEESMNSPCQVKQKQLRQVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
Db 61 DSYWDPNDEESMNSPCQVKQKQLRQVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
QY 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSGARNCSWKDAEYGLY 240  
Db 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSGARNCSWKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 15  
US-10-310-793-26  
; Sequence 26, Application US/10310793  
; Publication No. US20030198640A1

; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Zhang, Jun  
; APPLICANT: Wei, Ping  
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases  
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta  
; FILE REFERENCE: PF573  
; CURRENT APPLICATION NUMBER: US/10/310,793  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: 60/336,695  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 10/226,294  
; PRIOR FILING DATE: 2002-08-23  
; PRIOR APPLICATION NUMBER: 60/314,381  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 09/899,059  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/278,449  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 60/216,879  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 09/559,290  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/180,908  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 60/134,067  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: 60/132,227  
; PRIOR FILING DATE: 1999-05-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: human  
US-10-310-793-26

Query Match 100.0%; Score 281; DB 14; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272; Mismatches 0; Indels 0; Gaps 0;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60  
QY 61 DSYWDPNDEESMNSPCQVKQKQLRQVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
Db 61 DSYWDPNDEESMNSPCQVKQKQLRQVRKMLRTSEETISTVQEKQONISPLVREGPQ 120  
QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180  
QY 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSGARNCSWKDAEYGLY 240  
Db 181 FYIYISQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSGARNCSWKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 16  
US-10-279-687-8  
; Sequence 8, Application US/10279687  
; Publication No. US20030211509A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF

```
; FILE REFERENCE: 6255, US C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-687-8

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
   |||
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
   |||

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
   |||
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
   |||

QY 181 FYIYSQTYFRQEEIKENTKDKQWQVIYKYTSYDPDPILLMKSAARNCSWKDAEYGLY 240
   |||
Db 181 FYIYSQTYFRQEEIKENTKDKQWQVIYKYTSYDPDPILLMKSAARNCSWKDAEYGLY 240
   |||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
   |||
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
   |||

RESULT 17
US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532PI
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 281
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-5

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
   |||
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
   |||

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
   |||
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
   |||

QY 181 FYIYSQTYFRQEEIKENTKDKQWQVIYKYTSYDPDPILLMKSAARNCSWKDAEYGLY 240
   |||
Db 181 FYIYSQTYFRQEEIKENTKDKQWQVIYKYTSYDPDPILLMKSAARNCSWKDAEYGLY 240
   |||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
   |||
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
   |||

RESULT 18
US-10-333-712-1
; Sequence 1, Application US/10333712
; Publication No. US20040005314A1
; GENERAL INFORMATION:
; APPLICANT: Escandon, Enrique
; APPLICANT: Fox, Judith A.
; APPLICANT: Kelley, Sean K.
; APPLICANT: Xiang, Hong
; TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
; FILE REFERENCE: P1838R1
; CURRENT APPLICATION NUMBER: US/10/333,712
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: PCT/US01/23691
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,256
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-333-712-1

Query Match      100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
   |||
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
   |||

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
   |||

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
   |||
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVTHEKG 180
   |||

QY 181 FYIYSQTYFRQEEIKENTKDKQWQVIYKYTSYDPDPILLMKSAARNCSWKDAEYGLY 240
   |||
Db 181 FYIYSQTYFRQEEIKENTKDKQWQVIYKYTSYDPDPILLMKSAARNCSWKDAEYGLY 240
   |||
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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 24
US-10-381-160-5
; Sequence 5, Application US/10381160
; Publication No. US20040131587A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; TITLE OF INVENTION: METHOD FOR TREATMENT OF TUMORS USING COMBINATION THERAPY
; FILE REFERENCE: 2993-NO
; CURRENT APPLICATION NUMBER: US/10/381,160
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/242,868
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-381-160-5

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 25
US-10-755-889-210
; Sequence 210, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
```

```
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-210

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 26
US-10-491-326-1
; Sequence 1, Application US/10491326
; Publication No. US20040186051A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: Robert F. Kelley, Stephanie H. Lindstrom
; TITLE OF INVENTION: AP0-2 Ligand Variants and Uses Thereof
; FILE REFERENCE: P1858R1
; CURRENT APPLICATION NUMBER: US/10/491,326
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/326,622
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-491-326-1

Query Match 100.0%; Score 281; DB 16; Length 281;
Best Local Similarity 100.0%; Pred. No. 6.4e-272;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Qy 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
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Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
Qy 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240  
Db 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

## RESULT 27

US-10-810-063-2  
; Sequence 2, Application US/10810063  
; Publication No. US20040213764A1  
; GENERAL INFORMATION:  
; APPLICANT: WOLD, WILLIAM  
; APPLICANT: TOLLEFSON, ANN  
; TITLE OF INVENTION: ADENOVIRUS REPLICATION-COMPETENT VECTORS EXPRESSING  
; FILE REFERENCE: TRAIL  
; CURRENT APPLICATION NUMBER: US/10/810,063  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: 60/458,493  
; PRIOR FILING DATE: 2003-03-26  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-810-063-2

Query Match 100.0%; Score 281; DB 16; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDPNDEESMNSPCQVQWQRLVRLKMLRTSEETISTVQSKQNI SPLVRERGPQ 120  
Db 61 DDSYWDPNDEESMNSPCQVQWQRLVRLKMLRTSEETISTVQSKQNI SPLVRERGPQ 120  
Qy 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
Qy 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240  
Db 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

## RESULT 28

US-10-825-282-22  
; Sequence 22, Application US/10825282  
; Publication No. US20040224389A1  
; GENERAL INFORMATION:  
; APPLICANT: 3921-1-1-1  
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND  
; FILE REFERENCE: 3921-1-1-1  
; CURRENT APPLICATION NUMBER: US/10/825,282  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/456,357  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: 60/134,416

; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 09/087,195  
; PRIOR FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 08/378,507  
; PRIOR FILING DATE: 1995-01-26  
; PRIOR APPLICATION NUMBER: 08/250,478  
; PRIOR FILING DATE: 1994-05-27  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-825-282-22

Query Match 100.0%; Score 281; DB 16; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDPNDEESMNSPCQVQWQRLVRLKMLRTSEETISTVQSKQNI SPLVRERGPQ 120  
Db 61 DDSYWDPNDEESMNSPCQVQWQRLVRLKMLRTSEETISTVQSKQNI SPLVRERGPQ 120  
Qy 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIHEKG 180  
Qy 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240  
Db 181 FYYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDPILLMKSGARNCSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG 281

## RESULT 29

US-10-825-282-24  
; Sequence 24, Application US/10825282  
; Publication No. US20040224389A1  
; GENERAL INFORMATION:  
; APPLICANT: 3921-1-1-1  
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND  
; FILE REFERENCE: 3921-1-1-1  
; CURRENT APPLICATION NUMBER: US/10/825,282  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/456,357  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: 60/134,416  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 09/087,195  
; PRIOR FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 08/378,507  
; PRIOR FILING DATE: 1995-01-26  
; PRIOR APPLICATION NUMBER: 08/250,478  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-825-282-24

Query Match 100.0%; Score 281; DB 16; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Qy 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180  
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180  
Qy 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 30

US-10-399-116-5  
; Sequence 5, Application US/10399116  
; Publication No. US20040247563A1  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNEX CORPORATION  
; TITLE OF INVENTION: Method of Enhancing Lymphocyte-Mediated Immune Responses  
; FILE REFERENCE: 2995-WO  
; CURRENT APPLICATION NUMBER: US/10/399,116  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US 60/245,721  
; PRIOR FILING DATE: 2000-11-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-399-116-5

Query Match 100.0%; Score 281; DB 16; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Qy 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180  
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180  
Qy 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 31

US-10-688-845-36  
; Sequence 36, Application US/10688845  
; Publication No. US20040247578A1  
; GENERAL INFORMATION:  
; APPLICANT: Lotze, Michael T  
; APPLICANT: Tahara, Hideaki

; TITLE OF INVENTION: Methods And Reagents For Inducing Immunity  
; FILE REFERENCE: UPT-004  
; CURRENT APPLICATION NUMBER: US/10/688,845  
; CURRENT FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/418,865  
; PRIOR FILING DATE: 2002-10-15  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-688-845-36  
Query Match 100.0%; Score 281; DB 16; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Qy 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180  
Db 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180  
Qy 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIEKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 32

US-10-861-685-1  
; Sequence 1, Application US/10861685  
; Publication No. US20040253708A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669-22US03  
; CURRENT APPLICATION NUMBER: US/10/861,685  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US/09/584,031  
; PRIOR FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-861-685-1

Query Match 100.0%; Score 281; DB 16; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120  
Qy 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHGK 180

Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
QY 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSRNSCWKDAEYGLY 240  
Db 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSRNSCWKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 33

US-10-771-254-1  
; Sequence 1, Application US/10771254  
; Publication No. US20050020498A1  
; GENERAL INFORMATION:  
; Patin Docket Preview  
; APPLICANT: Flores, Heather  
; APPLICANT: Lin, Tanya P.  
; APPLICANT: Pai, Roger  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Matthews, Timothy C.  
; TITLE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS  
; FILE REFERENCE: P1857R1P1  
; CURRENT APPLICATION NUMBER: US/10/771,254  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/338,249  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: PCT/US02/36251  
; PRIOR FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-771-254-1

Query Match 100.0%; Score 281; DB 17; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
QY 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSRNSCWKDAEYGLY 240  
Db 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSRNSCWKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 34

US-10-855-559-2  
; Sequence 2, Application US/10855559  
; Publication No. US20050031593A1  
; GENERAL INFORMATION:  
; APPLICANT: Harding, Thomas  
; APPLICANT: Jooss, Karin  
; APPLICANT: Lalani, Alehad  
; APPLICANT: Donahue, Brian  
; TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of  
; One or More Anti-Angiogenic or Proapoptotic Genes

; FILE REFERENCE: 3802-094-27  
; CURRENT APPLICATION NUMBER: US/10/855,559  
; CURRENT FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: US 60/475,006  
; PRIOR FILING DATE: 2003-06-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-855-559-2

Query Match 100.0%; Score 281; DB 17; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
QY 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSRNSCWKDAEYGLY 240  
Db 181 FYIYSQTYFRQEEIKENTKNDKQVQIYKYTSYDPDPILLMKSRNSCWKDAEYGLY 240  
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

## RESULT 35

US-10-451-200-5  
; Sequence 5, Application US/10451200  
; Publication No. US20050048645A1  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNEX CORPORATION  
; TITLE OF INVENTION: METHOD OF TREATING OR PREVENTING DISEASE CHARACTERIZED BY CRYPTOCC  
; FILE REFERENCE: 2966-WO  
; CURRENT APPLICATION NUMBER: US/10/451,200  
; CURRENT FILING DATE: 2003-06-21  
; PRIOR APPLICATION NUMBER: US 60/259,653  
; PRIOR FILING DATE: 2001-01-04  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-451-200-5

Query Match 100.0%; Score 281; DB 17; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60  
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180  
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 36  
US-10-495-353-1  
; Sequence 1, Application US/10495353  
; Publication No. US2005080006A1  
; GENERAL INFORMATION:  
; APPLICANT: FLORES, Heather  
; APPLICANT: LIN, Tanya P.  
; APPLICANT: PAI, Roger  
; APPLICANT: SHAHROKH, Zahra  
; APPLICANT: MATTHEWS, Timothy  
; TITLE OF INVENTION: Apo-2 LIGAND/TRAIL FORMULATIONS  
; FILE REFERENCE: P1857R1  
; CURRENT APPLICATION NUMBER: US/10/495,353  
; CURRENT FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: PCT/US02/36251  
; PRIOR FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: US 60/338,249  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-495-353-1

Query Match 100.0%; Score 281; DB 17; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60  
Qy 61 DSDYWDNDDESMNSPCQVQWQRLQRLVRKMLRTSETISTVQEKQONISPLVRERGPO 120  
Db 61 DSDYWDNDDESMNSPCQVQWQRLQRLVRKMLRTSETISTVQEKQONISPLVRERGPO 120  
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 37  
US-10-652-979-1  
; Sequence 1, Application US/10652979  
; Publication No. US20050809958A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Schwalli, Ralph H.  
; TITLE OF INVENTION: Apo-2 Ligand  
; FILE REFERENCE: P0578P3C1  
; CURRENT APPLICATION NUMBER: US/10/652,979  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US 09/060,533

; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: US 09/007,886  
; PRIOR FILING DATE: 1998-01-15  
; PRIOR APPLICATION NUMBER: US 08/780,496  
; PRIOR FILING DATE: 1997-01-08  
; PRIOR APPLICATION NUMBER: US 60/009,755  
; PRIOR FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-652-979-1  
Query Match 100.0%; Score 281; DB 17; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6.4e-272;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKE 60  
Qy 61 DSDYWDNDDESMNSPCQVQWQRLQRLVRKMLRTSETISTVQEKQONISPLVRERGPO 120  
Db 61 DSDYWDNDDESMNSPCQVQWQRLQRLVRKMLRTSETISTVQEKQONISPLVRERGPO 120  
Qy 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240  
Db 181 FYIYSQTYFRFQBEIKENTKNDQMVOYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 38  
US-10-066-209-3  
; Sequence 3, Application US/10066209  
; Publication No. US20020115110A1  
; GENERAL INFORMATION:  
; APPLICANT: Brigham-Burke, Michael R.  
; APPLICANT: Young, Peter R.  
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND  
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2  
; FILE REFERENCE: GH-50030-D1  
; CURRENT APPLICATION NUMBER: US/10/066,209  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: 03/072,993  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/055,513  
; PRIOR FILING DATE: 1997-08-13  
; PRIOR APPLICATION NUMBER: 60/056,980  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/057,550  
; PRIOR FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 279  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-10-066-209-3

Query Match 99.3%; Score 279; DB 13; Length 279;  
Best Local Similarity 100.0%; Pred. No. 6.3e-270;  
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 MMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSGIACFLKEDD 62

Db 1 MMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTVYFTNKLQMDKYSKSGIACFLKEDD 60  
Qy 63 SYWDNDDESMNSPCQVQKWLRLVRKMLRTSETISTVQEKQONISPLVRERGPQV 122  
Db 61 SYWDNDDESMNSPCQVQKWLRLVRKMLRTSETISTVQEKQONISPLVRERGPQV 120  
Qy 123 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 182  
Db 121 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180  
Qy 183 YIYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDPDPILLMKSARNCSKDAEYGLYSI 242  
Db 181 YIYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDPDPILLMKSARNCSKDAEYGLYSI 240  
Qy 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281  
Db 241 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

## RESULT 39

US-10-738-423-10  
; Sequence 10, Application US/10738423  
; Publication No. US2004022938A1  
; GENERAL INFORMATION:  
; APPLICANT: Bermudes, G.  
; APPLICANT: King, I.  
; APPLICANT: Clairmont, C.  
; APPLICANT: Lin, S.  
; APPLICANT: Belcourt, M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES  
; FILE REFERENCE: 8002-059  
; CURRENT APPLICATION NUMBER: US/10/738,423  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: US/09/645,415  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 60/157,581  
; PRIOR FILING DATE: 1999-10-04  
; PRIOR APPLICATION NUMBER: 60/157,637  
; PRIOR FILING DATE: 1999-10-04  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion construct  
US-10-738-423-10

Query Match 86.1%; Score 242; DB 16; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5.5e-233;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 40 NELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCQVQKWLRLVRKMLRTSET 99  
Db 25 NELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCQVQKWLRLVRKMLRTSET 84  
Qy 100 ISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS 159  
Db 85 ISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS 144  
Qy 160 GHSFSLNHLRNGELVIEHKGYYIYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDPDP 219  
Db 145 GHSFSLNHLRNGELVIEHKGYYIYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDPDP 204  
Qy 220 ILLMKSARNCSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL 279  
Db 205 ILLMKSARNCSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL 264  
Qy 280 VG 281  
Db 265 VG 266

## RESULT 40

US-10-367-094-22  
; Sequence 22, Application US/10367094  
; Publication No. US20040170982A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer  
; FILE REFERENCE: 529452001500  
; CURRENT APPLICATION NUMBER: US/10/367,094  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 279  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-367-094-22

Query Match 84.7%; Score 238; DB 16; Length 279;  
Best Local Similarity 100.0%; Pred. No. 5.7e-229;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60  
Qy 61 DSDYWDNDDESMNSPCQVQKWLRLVRKMLRTSETISTVQEKQONISPLVRERGPQ 120  
Db 61 DSDYWDNDDESMNSPCQVQKWLRLVRKMLRTSETISTVQEKQONISPLVRERGPQ 120  
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180  
Qy 181 FYIYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDPDPILLMKSARNCSKDAEY 238  
Db 181 FYIYSQTYFRFQBEIKENTKNDKQVYIYKYTSYDPDPILLMKSARNCSKDAEY 238

## RESULT 41

US-09-855-544A-16  
; Sequence 16, Application US/09855544A  
; Patent No. US20020061525A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodrigo YELIN et al.  
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS  
; FILE REFERENCE: 27866-0173P  
; CURRENT APPLICATION NUMBER: US/09/855,544A  
; CURRENT FILING DATE: 2001-05-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 208  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-544A-16

Query Match 68.7%; Score 193; DB 9; Length 208;  
Best Local Similarity 100.0%; Pred. No. 3.9e-184;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCVAVTVYFTNKLQMDKYSGIACFLKE 60  
Qy 61 DSDYWDNDDESMNSPCQVQKWLRLVRKMLRTSETISTVQEKQONISPLVRERGPQ 120  
Db 61 DSDYWDNDDESMNSPCQVQKWLRLVRKMLRTSETISTVQEKQONISPLVRERGPQ 120  
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180

```
Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEK 180
Qy 181 FYIYSQTYFRFQ 193
Db 181 FYIYSQTYFRFQ 193

RESULT 42
US-10-652-244-11
; Sequence 11, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-10-652-244-11

Query Match 66.5%; Score 187; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.5e-178;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSEETISTVQEKQKNISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 67 TSEETISTVQEKQKNISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 126

Qy 155 ESSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQIYKYT 214
Db 127 ESSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQIYKYT 186

Qy 215 SYDPILLMKARSNCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 187 SYDPILLMKARSNCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246

Qy 275 FGAFLVG 281
Db 247 FGAFLVG 253

RESULT 43
US-10-652-244-13
; Sequence 13, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
```

```
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-10-652-244-13

Query Match 66.5%; Score 187; DB 15; Length 256;
Best Local Similarity 100.0%; Pred. No. 4.6e-178;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSEETISTVQEKQKNISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 70 TSEETISTVQEKQKNISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQIYKYT 214
Db 130 ESSRSGHSLNHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQIYKYT 189

Qy 215 SYDPILLMKARSNCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPILLMKARSNCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249

Qy 275 FGAFLVG 281
Db 250 FGAFLVG 256

RESULT 44
US-10-723-003-66
; Sequence 66, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-66

Query Match 66.5%; Score 187; DB 16; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.8e-178;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	95	TSEETISTVQKQNIISPLVRERGQORVAAHITGTRGRSNTLSSPNSKUEKALGRKINSW	154
Db	214	TSEETISTVQKQNIISPLVRERGQORVAAHITGTRGRSNTLSSPNSKUEKALGRKINSW	273
Qy	155	ESSRSGHSFLNLHLRNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQYIYKKT	214
Db	274	ESSRSGHSFLNLHLRNGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQYIYKKT	333
Qy	215	SYPPDILLMKSGARNCSWKDAEYGLIYSYQGGIFELKENDRIFVSVYTNHLLDMDHEASF	274
Db	334	SYPPDILLMKSGARNCSWKDAEYGLIYSYQGGIFELKENDRIFVSVYTNHLLDMDHEASF	393
Qy	275	FGAFLVG 281	
Db	394	FGAFLVG 400	

```

RESULT 45
US-10-389-223A-6
; Sequence 6, Application US/10389223A
; Publication No. US20040033511A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; APPLICANT: Wuest, Thomas
; APPLICANT: Moosmayer, Dieter
; TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytoki
; TITLE OF INVENTION: AMAize (Antibody-mediated Apoptosis Inducing Cytokines)
; FILE REFERENCE: 1708.002U51
; CURRENT APPLICATION NUMBER: US/10/389,223A
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of sequence 6: synthetic amino acid sequence of an
; OTHER INFORMATION: anti-body-cytokine AMAize fusion protein of the invention exempli
; OTHER INFORMATION: TRAIL-AMAize (40)
; FEATURE:
; OTHER INFORMATION: Stop codon: NT 1384-1386
; US-10-389-223A-6

```

RESULT 46  
US-10-389-223A-4  
; Sequence 4, Application US/10389223A  
; Publication No. US2004003511A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizenmaier, Klaus  
; APPLICANT: Wajant, Harald

```

1  APPLICANT: Wuest, Thomas
2  APPLICANT: Moosmayer, Dieter
3  TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokir
4  TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
5  FILE OF INVENTION: AMAIZE
6  FILE REFERENCE: 1708.002US1
7  CURRENT APPLICATION NUMBER: US/10/389.223A
8  CURRENT FILING DATE: 2003-03-14
9  NUMBER OF SEQ ID NOS: 12
10 SOFTWARE: PatentIn Ver. 2.1
11 SEQ ID NO 4
12 LENGTH: 480
13 TYPE: PRT
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: Description of sequence 4: synthetic amino acid sequence of an
17 OTHER INFORMATION: anti-body-cytokine AMAIZE fusion protein of the invention exemplif
18 OTHER INFORMATION: TRAIL-AMAIZE (OS4)
19 FEATURE:
20 OTHER INFORMATION: Stop codon: NT 1441-1443
21 US-10-389-223A-4

```

RESULT 47  
US-10-389-223A-2  
Sequence 2, Application US/10389223A  
Publication No. US2004003511A1  
GENERAL INFORMATION:  
APPLICANT: Pfizenmaier, Klaus  
APPLICANT: Wajant, Harald  
APPLICANT: Wuest, Thomas  
APPLICANT: Moosmayer, Dieter  
TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokir  
TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)  
FILE REFERENCE: 1708.002US1  
CURRENT APPLICATION NUMBER: US/10/389,223A  
CURRENT FILING DATE: 2003-03-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 2  
LENGTH: 614  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of sequence 2: synthetic amino acid sequence of an  
OTHER INFORMATION: anti-body-cytokine AMAIZE fusion protein of the invention exemplifi  
OTHER INFORMATION: TRAIL-AMAIZE (M80S4)  
FEATURE:  
OTHER INFORMATION: Stop codon: NT 1843-1845  
US-10-389-223A-2

Qy 95 TSEETISTVQKQNISPLVRRGPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154  
Db 428 TSEETISTVQKQNISPLVRRGPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 487  
Qy 155 ESSRSRSHSFLNLHLRNGELVIHKGFFYYISQTYFRFQBEIKENTKNDKQMVQIYKYT 214  
Db 488 ESSRSRSHSFLNLHLRNGELVIHKGFFYYISQTYFRFQBEIKENTKNDKQMVQIYKYT 547  
Qy 215 SYPPILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274  
Db 548 SYPPILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 607  
Qy 275 FGAFLVG 281  
Db 608 FGAFLVG 614

## RESULT 48

US-09-900-530A-10  
; Sequence 10, Application US/09900530A  
; Patent No. US20020128438A1  
; GENERAL INFORMATION:  
; APPLICANT: Seol, Dae-Wu  
; APPLICANT: Billiar, Timothy R.  
; TITLE OF INVENTION: DNA Cassette for the Production of  
; TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline  
; TITLE OF INVENTION: /doxycycline-inducible Adeno-Associated Virus Vector, Their  
; TITLE OF INVENTION: Combination and Use in Gene Therapy  
; FILE REFERENCE: 5006-1-002  
; CURRENT APPLICATION NUMBER: US/09/900.530A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: KR 2000-38441  
; PRIOR FILING DATE: 2000-07-06  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-900-530A-10

Query Match 59.8%; Score 168; DB 9; Length 168;  
Best Local Similarity 100.0%; Pred. No. 3e-159;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 VRERGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 173  
Db 1 VRERGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60  
Qy 174 LVIHEKGFYYISQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWK 233  
Db 61 LVIHEKGFYYISQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWK 120  
Qy 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 281  
Db 121 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 168

## RESULT 49

US-10-981-989-14  
; Sequence 14, Application US/10981989  
; Publication No. US20050113328A1  
; GENERAL INFORMATION:  
; APPLICANT: Devi, Gayathri  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Method and Antisense Compound for Potentiating Anti-Cancer Agents  
; FILE REFERENCE: 50450.8058.US00  
; CURRENT APPLICATION NUMBER: US/10/981.989  
; CURRENT FILING DATE: 2004-11-04  
; PRIOR APPLICATION NUMBER: 60/516,139  
; PRIOR FILING DATE: 2003-11-06  
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-981-989-14

Query Match 59.8%; Score 168; DB 17; Length 168;  
Best Local Similarity 100.0%; Pred. No. 3e-159;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 VRERGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 173  
Db 1 VRERGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 60  
Qy 174 LVIHEKGFYYISQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWK 233  
Db 61 LVIHEKGFYYISQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWK 120  
Qy 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 281  
Db 121 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 168

## RESULT 50

US-10-855-559-4  
; Sequence 4, Application US/10855559  
; Publication No. US20050031593A1  
; GENERAL INFORMATION:  
; APPLICANT: Harding, Thomas  
; APPLICANT: Jooss, Karin  
; APPLICANT: Lalani, Alshad  
; APPLICANT: Donahue, Brian  
; TITLE OF INVENTION: Method for Treating Cancer By Vector-Mediated Delivery of  
; TITLE OF INVENTION: One or More Anti-Angiogenic or Proapoptotic Genes  
; FILE REFERENCE: 3802-094-27  
; CURRENT APPLICATION NUMBER: US/10/855,559  
; CURRENT FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: US 60/475,006  
; PRIOR FILING DATE: 2003-06-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-855-559-4

Query Match 59.8%; Score 168; DB 17; Length 228;  
Best Local Similarity 100.0%; Pred. No. 3.9e-159;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 VRERGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 173  
Db 61 VRERGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGE 120  
Qy 174 LVIHEKGFYYISQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWK 233  
Db 121 LVIHEKGFYYISQTYFRFQBEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWK 180  
Qy 234 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 281  
Db 181 DAEGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPGAFLVG 228

## RESULT 51

US-10-723-003-64  
; Sequence 64, Application US/10723003  
; Publication No. US20040254108A1  
; GENERAL INFORMATION:  
; APPLICANT: Ma, Jing  
; APPLICANT: GUO, Yajun  
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF



```

; COMBLEN: SEQ ID NOS: 2.1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-7

Query Match          57.3%; Score 161; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ov      121 RVAAHITGTRGNTLTSSPNKQKALGRKINWESSRSGHSFSLNHLRNGELVVIHEKG 180

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Db 1 RVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEK 60
QY 181 FYIYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGL 240
Db 61 FYIYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGL 120
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 281
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 55
US-10-338-083-11
; Sequence 11, Application US/10338083
; Publication No. US2003016659A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Basell I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match 57.3%; Score 161; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 QVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEK 179
Db 1 QVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEK 60

QY 180 GFYIYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGL 239
Db 61 GFYIYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGL 120

QY 240 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 56
US-10-611-399-11
; Sequence 11, Application US/10611399
; Publication No. US20040170602A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Basell I.
; TITLE OF INVENTION: DOMINANT NEGATIVE PROTEINS AND METHODS THEREOF
; FILE REFERENCE: A-71273-3
; CURRENT APPLICATION NUMBER: US/10/611,399
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.2
```

```
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-399-11

Query Match 57.3%; Score 161; DB 16; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 QVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEK 179
Db 1 QVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEK 60

QY 180 GFYIYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGL 239
Db 61 GFYIYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGL 120

QY 240 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 57
US-10-794-751-11
; Sequence 11, Application US/10794751
; Publication No. US20050048626A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Thomason, Adam Read
; APPLICANT: Zhukovsky, Eugene Alexander
; TITLE OF INVENTION: BAFF VARIANTS AND METHODS THEREOF
; FILE REFERENCE: A-72175-1
; CURRENT APPLICATION NUMBER: US/10/794,751
; CURRENT FILING DATE: 2004-03-05
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 10/338,083
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/452,707
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/482,081
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/523,880
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 60/528,104
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-794-751-11

Query Match 57.3%; Score 161; DB 17; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.9e-152;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 QVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEK 179
Db 1 QVAAHITGTRGSRNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEK 60

QY 180 GFYIYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGL 239
Db 61 GFYIYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNSCWSDAEYGL 120

QY 240 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 58
US-10-778-890-10
; Sequence 10, Application US/10778890
```

```
; Publication No. US20050112596A1
; GENERAL INFORMATION:
; APPLICANT: TSCHOPP, JURG
; TITLE OF INVENTION: APRIL-A NOVEL PROTEIN WITH GROWTH EFFECTS
; FILE REFERENCE: A049 US
; CURRENT APPLICATION NUMBER: US/10/778,890
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US/09/520,489
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/19191
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/079,384
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/058,786
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-778-890-10

Query Match      56.2%; Score 158; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.8e-149;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGY 182
DB 1 AAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGY 60

QY 183 YIYSQTYRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLYSI 242
DB 61 YIYSQTYRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLYSI 120

QY 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
DB 121 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 158

RESULT 59
US-10-185-425-5
; Sequence 5, Application US/10185425
; Publication No. US20030053984A1
; GENERAL INFORMATION:
; APPLICANT: Apotech Research and Development Ltd.
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Holler, Nils
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
; FILE REFERENCE: 1708.001US1
; CURRENT APPLICATION NUMBER: US/10/185,425
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TRAIL-ACRP30
; NAME/KEY: DOMAIN
; LOCATION: (1)...(8)
; OTHER INFORMATION: Flag
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (9)...(16)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; FEATURE:
```

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; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17)...(108)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (109)...(110)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (111)...(296)
; OTHER INFORMATION: humanTRAIL aa 95-281
US-10-185-425-5

Query Match      55.5%; Score 156; DB 14; Length 296;
Best Local Similarity 100.0%; Pred. No. 4.8e-147;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGY 185
DB 141 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKGY 200

QY 186 SQTYRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLYSI 245
DB 201 SQTYRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWKSDAEYGLYSI 260

QY 246 GIFFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 281
DB 261 GIFFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 296

RESULT 60
US-10-871-776-5
; Sequence 5, Application US/10871776
; Publication No. US20040235117A1
; GENERAL INFORMATION:
; APPLICANT: Apotech Research and Development Ltd.
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Holler, Nils
; TITLE OF INVENTION: A Bimer or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
; FILE REFERENCE: 1708.001US1
; CURRENT APPLICATION NUMBER: US/10/871,776
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/10/185,425
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TRAIL-ACRP30
; NAME/KEY: DOMAIN
; LOCATION: (1)...(8)
; OTHER INFORMATION: Flag
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (9)...(16)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17)...(108)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; FEATURE:
```

```
; NAME/KEY: DOMAIN
; LOCATION: (109)...(110)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (111)...(296)
; OTHER INFORMATION: humanTRAIL aa 95-281
US-10-871-776-5

Query Match      55.5%; Score 156; DB 16; Length 296;
Best Local Similarity 100.0%; Pred. No. 4.8e-147; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 0;

QY 126 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIY 185
Db 141 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIY 200
QY 186 SQTFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKARSNSCWSKDAEYGLYSIYQG 245
Db 201 SQTFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKARSNSCWSKDAEYGLYSIYQG 260
QY 246 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 261 GIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 296

RESULT 61
US-10-781-866-29
; Sequence 29, Application US/10781866
; Publication No. US20040258681A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/10/781,866
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/569,611
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-29

Query Match      50.2%; Score 141; DB 16; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.8e-132; Indels 0; Gaps 0;
Matches 141; Conservative 0; Mismatches 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60
Db 25 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 84
QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONI SPLVRERGQP 120
Db 85 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQP 144
QY 121 RVAAHITGTRGRSNTLSSPNS 141
Db 145 RVAAHITGTRGRSNTLSSPNS 165

RESULT 62
US-09-855-544A-13
; Sequence 13, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-13

Query Match      50.2%; Score 141; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 3.9e-132; Indels 0; Gaps 0;
Matches 141; Conservative 0; Mismatches 0;

QY 141 SKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIYQTYFRFQEEIKENT 200
Db 106 SKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIYQTYFRFQEEIKENT 165
QY 201 KNDKQMVQYIYKYTSYDPDPILLMKARSNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 260
Db 166 KNDKQMVQYIYKYTSYDPDPILLMKARSNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV 225
QY 261 TNEHLIDMDHEASFFGAFLVG 281
Db 226 TNEHLIDMDHEASFFGAFLVG 246

RESULT 63
US-10-781-866-30
; Sequence 30, Application US/10781866
; Publication No. US20040258681A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/10/781,866
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/569,611
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-30

Query Match      47.7%; Score 134; DB 16; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.2e-125; Indels 0; Gaps 0;
Matches 134; Conservative 0; Mismatches 0;

QY 112 PLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLN 171
Db 122 PLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLN 181
QY 172 GELVIHEKGFYIYQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKARSNSCW 231
Db 182 GELVIHEKGFYIYQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKARSNSCW 241
QY 232 SKDAEYGLYSIYQG 245
Db 242 SKDAEYGLYSIYQG 255

RESULT 64
US-10-978-203-23
; Sequence 23, Application US/10978203
; Publication No. US20050112666A1
; GENERAL INFORMATION:
; APPLICANT: Chicheportiche, Yves
; APPLICANT: Browning, Jeffrey
; TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand
; FILE REFERENCE: A003
; CURRENT APPLICATION NUMBER: US/10/978,203
; CURRENT FILING DATE: 2004-10-29
```

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; PRIOR APPLICATION NUMBER: 60/023,541
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: 60/028,515
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: 60/040,820
; PRIOR FILING DATE: 1997-03-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 283
; TYPE: PRT
; ORGANISM: homo sapien
US-10-978-131-23

Query Match      46.3%; Score 130; DB 17; Length 283;
Best Local Similarity 100.0%; Pred. No. 4.3e-121;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 MQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQORVAAHITGTRGSNTLS 137
Db 82 MQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQORVAAHITGTRGSNTLS 141
QY 138 SPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKGFYIYSQTYFRQOEIK 197
Db 142 SPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKGFYIYSQTYFRQOEIK 201
QY 198 ENTNDKQMV 207
Db 202 ENTNDKQMV 211

RESULT 65
US-10-978-131-23
; Sequence 23, Application US/10978131
; Publication No. US20050118629A1
; GENERAL INFORMATION:
; APPLICANT: Chicheportiche, Yves
; APPLICANT: Browning, Jeffrey
; TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand
; FILE REFERENCE: A003
; CURRENT APPLICATION NUMBER: US/10/978,131
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/023,541
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: 60/028,515
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: 60/040,820
; PRIOR FILING DATE: 1997-03-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 283
; TYPE: PRT
; ORGANISM: homo sapien
US-10-978-131-23

Query Match      46.3%; Score 130; DB 17; Length 283;
Best Local Similarity 100.0%; Pred. No. 4.3e-121;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 MQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQORVAAHITGTRGSNTLS 137
Db 82 MQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQORVAAHITGTRGSNTLS 141
QY 138 SPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKGFYIYSQTYFRQOEIK 197
Db 142 SPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKGFYIYSQTYFRQOEIK 201
QY 198 ENTNDKQMV 207
Db 202 ENTNDKQMV 211
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RESULT 66
US-10-116-378-29
; Sequence 29, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29

Query Match      45.2%; Score 127; DB 13; Length 164;
Best Local Similarity 100.0%; Pred. No. 2.7e-118;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 GPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTH 177
Db 1 GPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTH 60
QY 178 EKGFYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPPDILLMKARNCSWKSADAY 237
Db 61 EKGFYIYSQTYFRQOEIKENTKNDKQMVQIYKYTSYPPDILLMKARNCSWKSADAY 120
QY 238 GLYSIQ 244
Db 121 GLYSIQ 127

RESULT 67
US-10-959-537-29
; Sequence 29, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/959,537
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/247,225
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-537-29

Query Match      45.2%; Score 127; DB 17; Length 164;
```

Best Local Similarity 100.0%; Pred. No. 2.7e-118;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 GPORVAAHITGRGSNTLSSPNSKNEALGKINSWESSRSGHSFLSNLHLRNGELVIH 177  
|||||  
Db 1 GPORVAAHITGRGSNTLSSPNSKNEALGKINSWESSRSGHSFLSNLHLRNGELVIH 60  
|||||

QY 178 EKGFFYYISQYFRFQEEIKENTKDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEY 237  
|||||  
Db 61 EKGFFYYISQYFRFQEEIKENTKDKQMVQYIYKTSYPPDILMKSRNSCWSKDAEY 120  
|||||

QY 238 GLYSIQ 244  
|||||  
Db 121 GLYSIQ 127  
|||||

RESULT 68  
US-10-006-305A-8  
; Sequence 8, Application US/10006305A  
; Publication No. US20050048476A1  
; GENERAL INFORMATION:  
; APPLICANT: PRUSSAK, CHARLES E.  
; APPLICANT: KIPPS, THOMAS J.  
; APPLICANT: CANTWELL, MARK J.  
; TITLE OF INVENTION: NOVEL CHIMERIC TNF LIGANDS  
; FILE REFERENCE: 041673-2092  
; CURRENT APPLICATION NUMBER: US/10/006,305A  
; CURRENT FILING DATE: 2001-12-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 8  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa  
; OTHER INFORMATION: polypeptide encoded by the DNA sequence of SEQ ID NO:4  
US-10-006-305A-8

Query Match 41.6%; Score 117; DB 17; Length 270;  
Best Local Similarity 100.0%; Pred. No. 4e-108;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCAVAVTVVYFTNLKQMDKYSGIACFLKE 60  
|||||  
Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCAVAVTVVYFTNLKQMDKYSGIACFLKE 60  
|||||

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQINISPLVR 117  
|||||  
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQINISPLVR 117  
|||||

RESULT 69  
US-09-855-544A-15  
; Sequence 15, Application US/09855544A  
; Patent No. US20020061525A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodrigo YELIN et al.  
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS  
; FILE REFERENCE: 2786-0173P  
; CURRENT APPLICATION NUMBER: US/09/855,544A  
; CURRENT FILING DATE: 2001-05-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-544A-15

Query Match 38.1%; Score 107; DB 9; Length 113;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCAVAVTVVYFTNLKQMDKYSGIACFLKE 60  
|||||  
Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCAVAVTVVYFTNLKQMDKYSGIACFLKE 60  
|||||

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQ 107  
|||||  
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQ 107  
|||||

RESULT 70  
US-09-855-544A-14  
; Sequence 14, Application US/09855544A  
; Patent No. US20020061525A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodrigo YELIN et al.  
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS  
; FILE REFERENCE: 2786-0173P  
; CURRENT APPLICATION NUMBER: US/09/855,544A  
; CURRENT FILING DATE: 2001-05-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-544A-14

Query Match 37.4%; Score 105; DB 9; Length 188;  
Best Local Similarity 100.0%; Pred. No. 2.8e-96;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCAVAVTVVYFTNLKQMDKYSGIACFLKE 60  
|||||

QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQ 105  
|||||  
Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQ 105  
|||||

RESULT 71  
US-09-855-544A-10  
; Sequence 10, Application US/09855544A  
; Patent No. US20020061525A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodrigo YELIN et al.  
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS  
; FILE REFERENCE: 2786-0173P  
; CURRENT APPLICATION NUMBER: US/09/855,544A  
; CURRENT FILING DATE: 2001-05-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-544A-10

Query Match 32.0%; Score 90; DB 9; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.5e-81;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 1 MAMMEVQGGPSLGTCTVLIVFTVLLQSLCAVAVTVVYFTNLKQMDKYSGIACFLKE 60  
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QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRK 90  
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Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRK 90  
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RESULT 72

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US-10-367-094-20
; Sequence 20, Application US/10367094
; Publication No. US20040170962A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-20

Query Match
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRLVRK 90
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRLVRK 90

RESULT 73
US-10-652-244-4
; Sequence 4, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-10-652-244-4

Query Match
Best Local Similarity 32.0%; Score 90; DB 15; Length 101;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRLVRK 90

US-10-662-429-2-oligo.rapb
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DB 61 DDSYWDPNDEESMNSPCWQVKWQLRLVRK 90

RESULT 74
US-10-781-866-32
; Sequence 32, Application US/10781866
; Publication No. US20040258681A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/10/781,866
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/569,611
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-32

Query Match
Best Local Similarity 32.0%; Score 90; DB 16; Length 120;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 25 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 84
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRLVRK 90
DB 85 DDSYWDPNDEESMNSPCWQVKWQLRLVRK 114

RESULT 75
US-10-781-866-31
; Sequence 31, Application US/10781866
; Publication No. US20040258681A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/10/781,866
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/569,611
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-866-31

Query Match
Best Local Similarity 32.0%; Score 90; DB 16; Length 122;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 60
DB 25 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLQMDKYSGIACFLKE 84
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRLVRK 90
DB 85 DDSYWDPNDEESMNSPCWQVKWQLRLVRK 114

Search completed: June 22, 2005, 07:05:30
Job time : 165 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2005, 06:39:23 ; Search time 42 Seconds  
(without alignments)  
499,438 Million cell updates/sec

Title: US-10-662-429-2  
Perfect score: 281  
Sequence: 1 MAMVEQGSPSLGQTCVLIV.....NEHLIDMDHEASFFGAFIVG 281

Scoring table: OLIGO  
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Searched: 513545 seqs, 74649064 residues

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	281	100.0	281	3	US-09-320-424-2
6	281	100.0	281	3	US-09-333-593A-6
7	281	100.0	281	4	US-09-157-864-11
8	281	100.0	281	4	US-09-825-563-2
9	281	100.0	281	4	US-09-919-039-118
10	281	100.0	281	4	US-09-582-450-1
11	281	100.0	281	4	US-09-934-465-1
12	281	100.0	281	4	US-10-011-125A-4
13	281	100.0	281	5	PCT-US96-10895-2
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15	187	66.5	253	3	US-09-320-424-11
16	187	66.5	253	4	US-09-825-563-11
17	187	66.5	256	3	US-09-320-424-13
18	187	66.5	256	4	US-09-825-563-13
19	174	61.9	177	3	US-09-105-343A-7
20	161	57.3	161	4	US-09-565-423-7
21	141	50.2	169	4	US-09-569-611C-29
22	134	47.7	271	4	US-09-569-611C-30
23	103	36.7	121	4	US-09-513-999C-7833
24	90	32.0	101	1	US-08-670-354-4
25	90	32.0	101	3	US-09-320-424-4
26	90	32.0	101	4	US-09-825-563-4
27	90	32.0	101	5	PCT-US96-10895-4

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29	90	32.0	122	4	US-09-569-611C-31	Sequence 31, Appl
30	85	30.2	85	4	US-09-632-287A-12	Sequence 12, Appl
31	24	8.5	59	4	US-09-621-976-6479	Sequence 1479, Ap
32	15	5.3	15	4	US-09-628-665-14	Sequence 64, Appl
33	15	5.3	19	4	US-09-628-665-32	Sequence 32, Appl
34	14	5.0	183	3	US-09-105-343A-8	Sequence 8, Appli
35	14	5.0	291	1	US-08-670-354-6	Sequence 6, Appli
36	14	5.0	291	3	US-09-320-424-6	Sequence 6, Appli
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39	12	4.3	87	4	US-09-632-287A-13	Sequence 13, Appl
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41	7	2.5	96	1	US-07-972-481-2	Sequence 2, Appli
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44	7	2.5	132	4	US-09-513-999C-5591	Sequence 5591, Ap
45	7	2.5	172	3	US-09-134-001C-5649	Sequence 5649, Ap
46	7	2.5	209	4	US-09-096-724B-8	Sequence 8, Appli
47	7	2.5	209	4	US-09-096-724B-24	Sequence 24, Appl
48	7	2.5	240	4	US-09-997-165-2	Sequence 2, Appli
49	7	2.5	274	4	US-09-489-039A-7595	Sequence 7595, Ap
50	7	2.5	384	4	US-09-270-767-35447	Sequence 35447, A
51	7	2.5	384	4	US-09-270-767-50664	Sequence 50664, A
52	7	2.5	400	4	US-09-302-626B-186	Sequence 186, App
53	7	2.5	429	4	US-09-198-452A-189	Sequence 189, App
54	7	2.5	432	4	US-09-438-185A-173	Sequence 173, App
55	7	2.5	487	4	US-09-248-796A-18251	Sequence 18251, A
56	7	2.5	554	4	US-08-909-125-6	Sequence 6, Appli
57	7	2.5	628	4	US-09-302-626B-183	Sequence 183, App
58	7	2.5	645	4	US-09-949-016-11022	Sequence 11022, A
59	7	2.5	700	4	US-09-831-642-34	Sequence 34, Appl
60	7	2.5	1532	4	US-09-302-626B-62	Sequence 62, Appl
61	7	2.5	1574	4	US-09-302-626B-179	Sequence 179, App
62	7	2.5	1978	4	US-09-302-626B-60	Sequence 60, Appl
63	7	2.5	2071	3	US-09-415-522-6	Sequence 6, Appli
64	6	2.1	6	4	US-09-628-665-13	Sequence 13, Appl
65	6	2.1	10	4	US-09-628-665-31	Sequence 31, Appl
66	6	2.1	24	4	US-09-612-402B-36	Sequence 26, Appl
67	6	2.1	25	4	US-09-270-767-57665	Sequence 57665, A
68	6	2.1	28	4	US-09-030-619-50	Sequence 50, Appl
69	6	2.1	46	3	US-08-858-207A-268	Sequence 268, App
70	6	2.1	54	4	US-09-270-767-42298	Sequence 42298, A
71	6	2.1	62	4	US-09-328-352-6548	Sequence 6548, Ap
72	6	2.1	62	4	US-09-513-999C-7381	Sequence 7381, Ap
73	6	2.1	76	4	US-09-270-767-33209	Sequence 32209, A
74	6	2.1	76	4	US-09-248-796A-27194	Sequence 27194, A
75	6	2.1	78	4	US-09-107-532A-5502	Sequence 5502, Ap
76	6	2.1	78	4	US-09-583-110-3425	Sequence 3425, Ap
77	6	2.1	83	4	US-09-543-681A-3440	Sequence 3440, Ap
78	6	2.1	84	4	US-09-513-999C-4910	Sequence 4910, Ap
79	6	2.1	85	4	US-09-248-796A-26098	Sequence 26098, A
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81	6	2.1	88	4	US-09-270-767-59036	Sequence 59036, A
82	6	2.1	88	4	US-09-513-999C-5744	Sequence 5744, Ap
83	6	2.1	95	4	US-09-270-767-42379	Sequence 42379, A
84	6	2.1	104	3	US-08-946-329A-99	Sequence 99, Appl
85	6	2.1	105	4	US-09-543-681A-8267	Sequence 8267, Ap
86	6	2.1	106	2	US-08-823-830B-4	Sequence 4, Appli
87	6	2.1	106	2	US-08-950-660-4	Sequence 4, Appli
88	6	2.1	106	4	US-09-157-452B-4	Sequence 4, Appli
89	6	2.1	106	4	US-08-454-899G-10	Sequence 10, Appl
90	6	2.1	106	5	PCT-US93-00030-4	Sequence 4, Appli
91	6	2.1	106	5	PCT-US93-00924-4	Sequence 4, Appli
92	6	2.1	108	4	US-09-270-767-38247	Sequence 38247, A
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94	6	2.1	111	4	US-09-270-767-38147	Sequence 38147, A
95	6	2.1	111	4	US-09-270-767-39454	Sequence 39454, A
96	6	2.1	111	4	US-09-270-767-53364	Sequence 53364, A
97	6	2.1	111	4	US-09-270-767-54671	Sequence 54671, A
98	6	2.1	112	4	US-09-270-767-33124	Sequence 33124, A
99	6	2.1	112	4	US-09-270-767-48341	Sequence 48341, A
100	6	2.1	114	4	US-09-621-976-5564	Sequence 5264, Ap

## ALIGNMENTS

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RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cycokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

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Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
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Qy      181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
Db      181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240

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Qy      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 2
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
Db      1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
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Qy      181 FYIYSQTYFRFQEEIKENTKNDKQVQYIYKYTSYDPDILLMKSAARNCSWKADEYGLY 240
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Db      241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 3
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: APO-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-780-496-1

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
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DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYSKSGIACFLKE 60
QY 61 DDSYNDPNDDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVVRERGQ 120
DB 61 DDSYNDPNDDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVVRERGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKDKQKVQYIYKTSYPPDILLMKSGARNCSWKSDAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKDKQKVQYIYKTSYPPDILLMKSGARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 4
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-10

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYSKSGIACFLKE 60
QY 61 DDSYNDPNDDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVVRERGQ 120
DB 61 DDSYNDPNDDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVVRERGQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVHEKG 180
QY 181 FYIYSQTYFRQOEIKENTKDKQKVQYIYKTSYPPDILLMKSGARNCSWKSDAEYGLY 240
DB 181 FYIYSQTYFRQOEIKENTKDKQKVQYIYKTSYPPDILLMKSGARNCSWKSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 5
US-09-320-424-2
; Sequence 2, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-320-424-2

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNKLKQMDKYSKSGIACFLKE 60
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Qy 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Qy 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Db 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYYISQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
Db 181 FYYISQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 6

US-09-333-593A-6  
; Sequence 6, Application US/09333593A  
; Patent No. 6313269  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH C.  
; APPLICANT: YOUNG, PETER R.  
; APPLICANT: MARSHALL, LISA A.  
; APPLICANT: ROSSHAK, AMY K.  
; APPLICANT: TAN, KONG B.  
; APPLICANT: TRUNEH, ALEMSEGED  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,  
; TITLE OF INVENTION: TR6  
; FILE REFERENCE: GH-50008-2  
; CURRENT APPLICATION NUMBER: US/09/333,593A  
; PRIOR FILING DATE: 1999-06-15  
; PRIOR APPLICATION NUMBER: 08/916,625  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 08/853,684  
; PRIOR FILING DATE: 1997-05-09  
; PRIOR APPLICATION NUMBER: 60/041,230  
; PRIOR FILING DATE: 1997-03-14  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-333-593A-6

Query Match 100.0%; Score 281; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6e-279;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Qy 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Db 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYYISQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
Db 181 FYYISQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 7

US-09-157-864-11  
; Sequence 11, Application US/09157864  
; Patent No. 6440694  
; GENERAL INFORMATION:  
; APPLICANT: Bienkowski, Michael J  
; APPLICANT: Mills, Cynthia J  
; APPLICANT: Jones, David A  
; TITLE OF INVENTION: TNF-Related Death Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/157,864  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerber, Lori L.  
; REGISTRATION NUMBER: 41,113  
; REFERENCE/DOCKET NUMBER: 6111.N CN1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616/833-0974  
; TELEFAX: 616/833-8897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-157-864-11

Query Match 100.0%; Score 281; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6e-279;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYKSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYKSGIACFLKE 60  
Qy 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Qy 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Db 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180  
Qy 181 FYYISQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
Db 181 FYYISQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240  
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 8

US-09-825-563-2  
; Sequence 2, Application US/09825563  
; Patent No. 6521228

```

; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
;
US-09-825-563-2

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RAAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RAAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 10
US-09-582-450-1
; Sequence 1, Application US/09582450
; Patent No. 6740739
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Kelley, Robert F.
; APPLICANT: O'Connell, Mark P.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Schwalli, Ralph H.
; TITLE OF INVENTION: Apo-2 Ligand
; FILE REFERENCE: P0978P4
; CURRENT APPLICATION NUMBER: US/09/582,450
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/007,886
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 09/060,533
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-582-450-1

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RAAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RAAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

US-09-919-039-118
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
;
US-09-825-563-2

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RAAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RAAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQMVQYIYKTSYPPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9
US-09-919-039-118
; Sequence 118, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 059509CD1

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Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 11

US-09-934-465-1  
; Sequence 1, Application US/09934465  
; Patent No. 6746668  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669-22US03  
; CURRENT APPLICATION NUMBER: US/09/934,465  
; CURRENT FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: 08/584,031  
; PRIOR FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-934-465-1

Query Match 100.0%; Score 281; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6e-279;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLKQMDKYSGIACFLKE 60  
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLKQMDKYSGIACFLKE 60  
Qy 61 DDSYWDNDPNDSESMNSPCQVQKWLRLVTKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDNDPNDSESMNSPCQVQKWLRLVTKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180  
Qy 181 FYIYSQTYFRFOBEIKENTKNDQMVOYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDQMVOYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 12

US-10-011-125A-4  
; Sequence 4, Application US/10011125A  
; Patent No. 6828121  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Christina Yu-Ching  
; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
; FILE REFERENCE: P1804R1  
; CURRENT APPLICATION NUMBER: US/10/011,125A  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/256,162  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 4  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-011-125A-4

Query Match 100.0%; Score 281; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6e-279;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLKQMDKYSGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLKQMDKYSGIACFLKE 60  
Qy 61 DDSYWDNDPNDSESMNSPCQVQKWLRLVTKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Db 61 DDSYWDNDPNDSESMNSPCQVQKWLRLVTKMLRTSEETISTVQEKQONISPLVRERGQ 120  
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180  
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180  
Qy 181 FYIYSQTYFRFOBEIKENTKNDQMVOYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240  
Db 181 FYIYSQTYFRFOBEIKENTKNDQMVOYIYKYTSYDPDPILLMKSARNCSWSDAEYGLY 240  
Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281  
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

## RESULT 13

PCT-US96-10895-2  
; Sequence 2, Application PC/TUS9610895  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation.  
; TITLE OF INVENTION: Cytokine That Induces Apoptosis  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.5.2  
; SOFTWARE: Microsoft Word, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/10895  
; FILING DATE: 25-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/496,632  
; FILING DATE: 29-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/548,368  
; FILING DATE: 01-NOV-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2835-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-10895-2

Query Match 100.0%; Score 281; DB 5; Length 281;  
Best Local Similarity 100.0%; Pred. No. 6e-279;  
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLKQMDKYSGIACFLKE 60



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Db 1 MAMVEVQGGPSLGGTCLVLIIVFTVLLQSLCAVATYVYFTNELKQMDKYKSGIACFLKE 60
Qy 61 DSDYWDPNDESMNSPCWQVKQLRQLVRLKMLRTSEETISTVQEKQKQNISPLVREGRPQ 120
Db 61 DSDYWDPNDESMNSPCWQVKQLRQLVRLKMLRTSEETISTVQEKQKQNISPLVREGRPQ 120
Qy 121 RVAAHITGTRGNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVHKG 180
Db 121 RVAAHITGTRGNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVHKG 180
Qy 181 FYIYSQTYFRFQEBIKENTKNDKQKVQYIYKTSYPPDPILLMKSNCSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEBIKENTKNDKQKVQYIYKTSYPPDPILLMKSNCSKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFLVG 281

RESULT 14
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3

Query Match 99.3%; Score 279; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 6.6e-277;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVATYVYFTNELKQMDKYKSGIACFLKEDD 62
Db 1 MMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVATYVYFTNELKQMDKYKSGIACFLKEDD 60
Qy 63 SYWDPNDESMNSPCWQVKQLRQLVRLKMLRTSEETISTVQEKQKQNISPLVREGRPQV 122
Db 61 SYWDPNDESMNSPCWQVKQLRQLVRLKMLRTSEETISTVQEKQKQNISPLVREGRPQV 120
Qy 123 AAHITGTRGNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVHKG 182
Db 121 AAHITGTRGNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGELVHKG 180
Qy 183 YIYQTYFRFQEBIKENTKNDKQKVQYIYKTSYPPDPILLMKSNCSKDAEYGLY 242
Db 181 YIYQTYFRFQEBIKENTKNDKQKVQYIYKTSYPPDPILLMKSNCSKDAEYGLY 240
Qy 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFLVG 281
Db 241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFPFGAFLVG 279

RESULT 15
US-09-320-424-11
; Sequence 11, Application US/09320424
```

```
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match 66.5%; Score 187; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.4e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSEETISTVQEKQKQNISPLVREGRPQVAAHITGTRGNTLSSPNSKNEALGRKINSW 154
Db 67 TSEETISTVQEKQKQNISPLVREGRPQVAAHITGTRGNTLSSPNSKNEALGRKINSW 126
Qy 155 ESSRSGHSFSLNHLRNGELVHKG 214
Db 127 ESSRSGHSFSLNHLRNGELVHKG 214
Qy 215 SYDPILLMKSNCSKDAEYGLY 274
Db 187 SYDPILLMKSNCSKDAEYGLY 246
Qy 275 FGAFLVG 281
Db 247 FGAFLVG 253

RESULT 16
US-09-825-563-11
; Sequence 11, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
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; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-11

Query Match      66.5%; Score 187; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.4e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 67 TSETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 126

Qy 155 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYT 214
Db 127 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYT 186

Qy 215 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 187 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246

Qy 275 FGAFVLVG 281
Db 247 FGAFVLVG 253

RESULT 17
US-09-320-424-13
; Sequence 13, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-13

Query Match      66.5%; Score 187; DB 3; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 70 TSETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYT 214
Db 130 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYT 189

Qy 215 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249

Qy 275 FGAFVLVG 281
Db 247 FGAFVLVG 253

US-09-320-424-13

Query Match      66.5%; Score 187; DB 3; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 70 TSETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYT 214
Db 130 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYT 189

Qy 215 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249

Qy 275 FGAFVLVG 281
Db 247 FGAFVLVG 253

US-09-320-424-13
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Db 250 FGAFVLVG 256

RESULT 18
US-09-825-563-13
; Sequence 13, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-13

Query Match      66.5%; Score 187; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 70 TSETISTVQEKQONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYT 214
Db 130 ESSRSGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYT 189

Qy 215 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249

Qy 275 FGAFVLVG 281
Db 250 FGAFVLVG 256

US-09-825-563-13

RESULT 19
US-09-105-343A-7
; Sequence 7, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 26
US-09-825-563-4
; Sequence 4, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-09-825-563-4

Query Match 32.0%; Score 90; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.9e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 27
PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
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SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-4

Query Match 32.0%; Score 90; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.9e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90

RESULT 28
US-09-569-611C-32
; Sequence 32, Application US/09569611C
; Patent No. 6720182
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-32

Query Match 32.0%; Score 90; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.5e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDKYSKSGIACFLKE 60
DB 25 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLQMDKYSKSGIACFLKE 84
QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
DB 85 DDSYWDPNDEESMNSPCWQVKWQLRQLVRK 114
```

```
RESULT 29
US-09-569-611C-31
; APPLICANT: Savitzky et al.
; TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS
; FILE REFERENCE: 2786-0151P
; CURRENT APPLICATION NUMBER: US/09/569,611C
; CURRENT FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-611C-31

Query Match      32.0%; Score 90; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 4.6e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 60
DB 25 MAMVEVQGGPSLGQTCVLIVITVLLQSLCVAVTVYFTNELKQMDKYSGIACFLKE 84

QY 61 DSYWDPNDEESMNSPCWQKQLRQLVRK 90
DB 85 DSYWDPNDEESMNSPCWQKQLRQLVRK 114

RESULT 30
US-09-632-287A-12
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fm, A No. 6521422e1 Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/3550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-632-287A-12

Query Match      30.2%; Score 85; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 4.3e-79;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ERGPORVAHITGTRSNLTSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 175
DB 1 ERGPORVAHITGTRSNLTSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 60

QY 176 IHEKGFYIYSQTYFRFQEEIKENT 200
DB 61 IHEKGFYIYSQTYFRFQEEIKENT 85

RESULT 31
US-09-621-976-6479
; APPLICANT: Dumas Milne Edwards, J.B.
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE:
; NUMBER OF SEQ ID NOS:
; SOFTWARE:
; SEQ ID NO:
; LENGTH:
; TYPE:
; ORGANISM:
US-09-621-976-6479

Query Match      5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFOEEIKENTKNDKQ 205
DB 1 RFOEEIKENTKNDKQ 15

RESULT 32
US-09-628-665-14
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-14

Query Match      5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFOEEIKENTKNDKQ 205
DB 1 RFOEEIKENTKNDKQ 15

RESULT 33
US-09-628-665-32
; APPLICANT: Dumas Milne Edwards, J.B.
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE:
; NUMBER OF SEQ ID NOS:
; SOFTWARE:
; SEQ ID NO:
; LENGTH:
; TYPE:
; ORGANISM:
US-09-628-665-32

Query Match      5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFOEEIKENTKNDKQ 205
DB 1 RFOEEIKENTKNDKQ 15
```

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; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6479
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 27
; OTHER INFORMATION: Xaa = Glu, Gln
; NAME/KEY: UNSURE
; LOCATION: 34
; OTHER INFORMATION: Xaa = Glu, Val
; NAME/KEY: UNSURE
; LOCATION: 33.57
; OTHER INFORMATION: Xaa = Leu, Pro
; NAME/KEY: UNSURE
; LOCATION: 25.32
; OTHER INFORMATION: Xaa = Leu, Val
US-09-621-976-6479

Query Match      8.5%; Score 24; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 6.9e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGGPSLGQTCVLIVIFTV 24
DB 1 MAMVEVQGGPSLGQTCVLIVIFTV 24

RESULT 32
US-09-628-665-14
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-14

Query Match      5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFOEEIKENTKNDKQ 205
DB 1 RFOEEIKENTKNDKQ 15

RESULT 33
US-09-628-665-32
; APPLICANT: Dumas Milne Edwards, J.B.
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE:
; NUMBER OF SEQ ID NOS:
; SOFTWARE:
; SEQ ID NO:
; LENGTH:
; TYPE:
; ORGANISM:
US-09-628-665-32

Query Match      5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFOEEIKENTKNDKQ 205
DB 1 RFOEEIKENTKNDKQ 15
```

APPLICANT: Greene, Mark I.  
APPLICANT: Murali, Ramachandran  
APPLICANT: Kinoshita, Masahiko  
TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity  
FILE REFERENCE: UPN3831  
CURRENT APPLICATION NUMBER: US/09/628,665  
CURRENT FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/146,094  
PRIOR FILING DATE: 1999-07-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence  
US-09-628-665-32

Query Match 5.3%; Score 15; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.9e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 RFQEEIKENTKNDKQ 205  
DB 3 RFQEEIKENTKNDKQ 17

RESULT 34  
US-09-105-343A-8  
Sequence 8, Application US/09105343A  
Patent No. 6207642  
GENERAL INFORMATION:  
APPLICANT: WILEY, S.R.  
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-6050  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/105,343A  
FILING DATE: 12-FEB-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/02859  
FILING DATE: 12-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: BECKER, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6048.US.P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-935-1729  
TELEFAX: 847-938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 183 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6207642e  
US-09-105-343A-8

Query Match 5.0%; Score 14; DB 3; Length 183;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKTSYDPPI 220  
DB 109 VQYIYKTSYDPPI 122

RESULT 35  
US-08-670-354-6  
Sequence 6, Application US/08670354  
Patent No. 5763223  
GENERAL INFORMATION:  
APPLICANT: Steven R. Wiley and  
APPLICANT: Raymond G. Goodwin.  
TITLE OF INVENTION: Cytokine That Induces Apoptosis  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.5.2  
SOFTWARE: Microsoft Word, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/670,354  
FILING DATE: 25-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/496,632  
FILING DATE: 29-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/548,368  
FILING DATE: 01-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2835-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 291 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-670-354-6

Query Match 5.0%; Score 14; DB 1; Length 291;  
Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKTSYDPPI 220  
DB 217 VQYIYKTSYDPPI 230

RESULT 36  
US-09-320-424-6  
Sequence 6, Application US/09320424  
Patent No. 6284236  
GENERAL INFORMATION:  
APPLICANT: Wiley, Steven R.



; LENGTH: 87

; TYPE: PRT  
; ORGANISM: Mouse  
US-09-632-287A-13

Query Match 4.3%; Score 12; DB 4; Length 87;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 YIYSQTYFRFOE 194  
|||||  
DB 65 YIYSQTYFRFOE 76  
|||||

## RESULT 40

US-09-902-540-14513

; Sequence 14513, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 14513  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus

US-09-902-540-14513

Query Match 2.8%; Score 8; DB 4; Length 70;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 VAAHITGT 129  
|||||  
DB 4 VAAHITGT 11  
|||||

## RESULT 41

US-07-972-481-2

; Sequence 2, Application US/07972481  
; Patent No. 5578453  
; GENERAL INFORMATION:  
; APPLICANT: McDONALD, PETER J  
; APPLICANT: JOHNSON, ALAN M  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TOXOPLASMA ANTIGENS AND  
; TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
; STREET: 8110 GATEHOUSE ROAD  
; CITY: FALLS CHURCH  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/972,481  
; FILING DATE: 12-APR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: INTERNATIONAL PCT/AU91/00347  
; FILING DATE: 09-AUG-1991

; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 446-102PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 96 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-972-481-2

Query Match 2.5%; Score 7; DB 1; Length 96;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FOEEIKE 198  
|||||  
DB 2 FOEEIKE 8  
|||||

## RESULT 42

US-09-513-999C-5589

; Sequence 5589, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5589  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 116  
; OTHER INFORMATION: Xaa=Ala or Asp or Glu

Query Match 2.5%; Score 7; DB 4; Length 132;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199  
|||||  
DB 9 QEEIKEN 15  
|||||

## RESULT 43

US-09-513-999C-5590

; Sequence 5590, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5590  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 116  
; OTHER INFORMATION: Xaa=Ala or Asp or Glu  
US-09-513-999C-5590

Query Match 2.5%; Score 7; DB 4; Length 132;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QBEIKEN 199  
Db 9 QBEIKEN 15

## RESULT 44

US-09-513-999C-5591  
; Sequence 5591, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5591  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 116  
; OTHER INFORMATION: Xaa=Ala or Asp or Glu  
US-09-513-999C-5591

Query Match 2.5%; Score 7; DB 4; Length 132;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QBEIKEN 199  
Db 9 QBEIKEN 15

## RESULT 45

US-09-134-001C-5649  
; Sequence 5649, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5649  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5649

Query Match 2.5%; Score 7; DB 3; Length 172;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278  
Db 105 ASFFGAF 111

## RESULT 46

US-09-096-724B-8  
; Sequence 8, Application US/09096724B  
; Patent No. 6548290  
; GENERAL INFORMATION:  
; APPLICANT: McGarry, Thomas J.  
; APPLICANT: Kroll, Kristen  
; APPLICANT: Kirschner, Marc W.  
; TITLE OF INVENTION: Geminin Gene and Protein  
; FILE REFERENCE: 0725.1055-001  
; CURRENT APPLICATION NUMBER: US/09/096,724B  
; CURRENT FILING DATE: 1998-06-11  
; PRIOR APPLICATION NUMBER: 60/085,371  
; PRIOR FILING DATE: 1998-05-13  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: human  
US-09-096-724B-8

Query Match 2.5%; Score 7; DB 4; Length 209;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QBEIKEN 199  
Db 9 QBEIKEN 15

## RESULT 47

US-09-096-724B-24  
; Sequence 24, Application US/09096724B  
; Patent No. 6548290  
; GENERAL INFORMATION:  
; APPLICANT: McGarry, Thomas J.  
; APPLICANT: Kroll, Kristen  
; APPLICANT: Kirschner, Marc W.  
; TITLE OF INVENTION: Geminin Gene and Protein  
; FILE REFERENCE: 0725.1055-001  
; CURRENT APPLICATION NUMBER: US/09/096,724B  
; CURRENT FILING DATE: 1998-06-11  
; PRIOR APPLICATION NUMBER: 60/085,371  
; PRIOR FILING DATE: 1998-05-13  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: human  
US-09-096-724B-24

Query Match 2.5%; Score 7; DB 4; Length 209;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 193 QBEIKEN 199
Db 9 QBEIKEN 15

RESULT 48
US-09-997-165-2
; Sequence 2, Application US/09997165
; Patent No. 6762030
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Fanelow, William C.
; TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF
; FILE REFERENCE: 2913-US
; CURRENT APPLICATION NUMBER: US/09/997,165
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: PCT/US00/14612
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,450
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-165-2

Query Match 2.5%; Score 7; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 NTLSSPN 140
Db 231 NTLSSPN 237

RESULT 49
US-09-489-039A-7595
; Sequence 7595, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7595
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7595

Query Match 2.5%; Score 7; DB 4; Length 274;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 ISPLVRE 116
Db 117 ISPLVRE 123

RESULT 50
US-09-270-767-35447
; Sequence 35447, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
```

---

```
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35447
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35447

Query Match 2.5%; Score 7; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 VREGRGPQ 120
Db 56 VREGRGPQ 62

RESULT 51
US-09-270-767-50664
; Sequence 50664, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50664
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50664

Query Match 2.5%; Score 7; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 VREGRGPQ 120
Db 56 VREGRGPQ 62

RESULT 52
US-09-302-626B-186
; Sequence 186, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIRO159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 400
; TYPE: PRT
```

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ORF114a  
; NAME/KEY: SITE  
; LOCATION: (58)  
; OTHER INFORMATION: place-holder  
; NAME/KEY: SITE  
; LOCATION: (105)  
; OTHER INFORMATION: place-holder  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: place-holder  
; NAME/KEY: SITE  
; LOCATION: (139)  
; OTHER INFORMATION: place-holder  
; NAME/KEY: SITE  
; LOCATION: (179)  
; OTHER INFORMATION: place-holder  
; NAME/KEY: SITE  
; LOCATION: (209)  
; OTHER INFORMATION: place-holder  
; NAME/KEY: SITE  
; LOCATION: (344)..(355)  
; OTHER INFORMATION: place-holder  
US-09-302-626B-186

Query Match 2.5%; Score 7; DB 4; Length 400;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHTGT 129  
Db 322 AAHTGT 328

## RESULT 53

US-09-198-452A-189  
; Sequence 189, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffois, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 189  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-189

Query Match 2.5%; Score 7; DB 4; Length 429;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161  
Db 248 ESSRSRGH 254

## RESULT 54

US-09-438-185A-173  
; Sequence 173, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 173  
; LENGTH: 432  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: CFP0171  
US-09-438-185A-173

Query Match 2.5%; Score 7; DB 4; Length 432;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161  
Db 251 ESSRSRGH 257

## RESULT 55

US-09-248-796A-18251  
; Sequence 18251, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18251  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-18251

Query Match 2.5%; Score 7; DB 4; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SLGQTCV 17  
Db 285 SLGQTCV 291

## RESULT 56

US-08-909-125-6  
; Sequence 6, Application US/08909125  
; Patent No. 6495737  
; GENERAL INFORMATION:  
; APPLICANT: KLESSIG, DANIEL  
; APPLICANT: GUO, AILAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMPROVING  
; TITLE OF INVENTION: SALICYLIC ACID-INDEPENDENT SYSTEMIC ACQUIRED DISEASE RESISTANCE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
; STREET: 1601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA

```
/ COUNTRY: USA
/ ZIP: 19103-2307
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/909,125
/ FILING DATE: 11-AUG-1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/024,033
/ FILING DATE: 12-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: JANET E. REED, PH.D.
/ REGISTRATION NUMBER: 36,252
/ REFERENCE/DOCKET NUMBER: Rutgers 97-0009
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-563-4100
/ TELEFAX: 215-563-4044
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 554 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ US-08-909-125-6
```

```
Query Match 2.5%; Score 7; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 145 KALGRKI 151
Db 477 KALGRKI 483
```

```
RESULT 57
US-08-909-125-6
; Sequence 183, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 183
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF114a
; NAME/KEY: SITE
; LOCATION: (47)..(73)
; OTHER INFORMATION: place-holder
; NAME/KEY: SITE
; LOCATION: (85)
```

```
/ OTHER INFORMATION: place-holder
/ NAME/KEY: SITE
/ LOCATION: (296)
/ OTHER INFORMATION: place-holder
/ NAME/KEY: SITE
/ LOCATION: (343)
/ OTHER INFORMATION: place-holder
/ NAME/KEY: SITE
/ LOCATION: (352)
/ OTHER INFORMATION: place-holder
/ NAME/KEY: SITE
/ LOCATION: (377)
/ OTHER INFORMATION: place-holder
/ NAME/KEY: SITE
/ LOCATION: (417)
/ OTHER INFORMATION: place-holder
/ NAME/KEY: SITE
/ LOCATION: (447)
/ OTHER INFORMATION: place-holder
/ NAME/KEY: SITE
/ LOCATION: (582)..(593)
/ OTHER INFORMATION: place-holder
/ US-09-302-626B-183
```

```
Query Match 2.5%; Score 7; DB 4; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 123 AAHITGT 129
Db 560 AAHITGT 566
```

## RESULT 58

```
US-09-949-016-11022
; Sequence 11022, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11022
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11022
```

```
Query Match 2.5%; Score 7; DB 4; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 23 TVLQSL 29
Db 278 TVLQSL 284
```

## RESULT 59

```
US-09-831-642-34
; Sequence 34, Application US/09831642
; Patent No. 6635751
; GENERAL INFORMATION:
; APPLICANT: HAZE, Kiyosuke et al.
```

```

; TITLE OF INVENTION: ENDOPLASMIC RETICULUM STRESS TRANSCRIPTION FACTORS ATF6 AND CREB-
; FILE REFERENCE: 1422-0474P
; CURRENT APPLICATION NUMBER: US/09/831,642
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-831-642-34

Query Match      2.5%; Score 7; DB 4; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 TVLQSL 29
DB      263 TVLQSL 269

RESULT 60
US-09-302-626B-62
; Sequence 62, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 1532
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (68)..(73)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (85)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (296)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (343)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (352)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (377)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (417)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (477)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (665)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (693)..(694)

;
; TITLE OF INVENTION: unknown
; NAME/KEY: SITE
; LOCATION: (781)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (805)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (903)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (922)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (959)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (963)..(965)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (985)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1157)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1164)..(1165)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1175)..(1176)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1220)..(1221)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1249)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1270)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1300)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1447)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1508)
; OTHER INFORMATION: unknown
; NAME/KEY: SITE
; LOCATION: (1526)
; OTHER INFORMATION: unknown
US-09-302-626B-62

Query Match      2.5%; Score 7; DB 4; Length 1532;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      123 AAHTGT 129
DB      560 AAHTGT 566

RESULT 61
US-09-302-626B-179
; Sequence 179, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
```

```
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF114-1
US-09-302-626B-179

Query Match      2.5%; Score 7; DB 4; Length 1574;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
Db      560 AAHITGT 566

RESULT 62
US-09-302-626B-60
; Sequence 60, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 1978
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-302-626B-60

Query Match      2.5%; Score 7; DB 4; Length 1978;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
Db      560 AAHITGT 566

RESULT 63
US-09-415-522-6
; Sequence 6, Application US/09415522A
; Patent No. 6291660
; GENERAL INFORMATION:
; APPLICANT: Gaffney, Thomas
; APPLICANT: Wendland, Juergen
; APPLICANT: Philippsen, Peter
; TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth And
; FILE REFERENCE: CGC2046
; CURRENT APPLICATION NUMBER: US/09/415,522A
; CURRENT FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0

; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF114-1
US-09-302-626B-179

Query Match      2.5%; Score 7; DB 4; Length 1574;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
Db      560 AAHITGT 566

RESULT 62
US-09-302-626B-60
; Sequence 60, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 1978
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-302-626B-60

Query Match      2.1%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSGHS 162
Db      1 SRSGHS 6

RESULT 65
US-09-628-665-31
; Sequence 31, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-31

Query Match      2.1%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSGHS 162
Db      1 SRSGHS 6

RESULT 65
US-09-628-665-31
; Sequence 31, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-31

Query Match      2.1%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSGHS 162
Db      1 SRSGHS 6
```



```
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSQHS 162
Db 3 SRSQHS 8

RESULT 66
US-09-612-402B-26
; Sequence 26, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; Patent No. 6642023
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612,402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Chlamydia sp.
US-09-612-402B-26

Query Match 2.1%; Score 6; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 LSNLHL 169
Db 8 LSNLHL 13

RESULT 67
US-09-270-767-57665
; Sequence 57665, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57665
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-57665

Query Match 2.1%; Score 6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 GRKINS 153
Db 17 GRKINS 22

RESULT 68
US-09-030-619-50
; Sequence 50, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert

; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 66081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin Analogue
US-09-030-619-50

Query Match 2.1%; Score 6; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 RKMILR 94
Db 11 RKMILR 16

RESULT 69
US-08-858-207A-268
; Sequence 268, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 268:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6348328e
US-08-858-207A-268

Query Match          2.1%; Score 6; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 FTNELK 43
Db 19 FTNELK 24

RESULT 70
US-09-270-767-42298
; Sequence 42298, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42298
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42298

Query Match          2.1%; Score 6; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TGRSN 134
Db 29 TGRSN 34

RESULT 71
US-09-328-352-6548
; Sequence 6548, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6548
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6548

Query Match          2.1%; Score 6; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 IACFLK 59
Db 1 IACFLK 6

RESULT 72
US-09-513-999C-7381
; Sequence 7381, Application US/09513999C
; Patent No. 6783961
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7381
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 31
; OTHER INFORMATION: Xaa=Glu or Lys
US-09-513-999C-7381

Query Match          2.1%; Score 6; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 SNLHLR 170
Db 25 SNLHLR 30

RESULT 73
US-09-270-767-32209
; Sequence 32209, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32209
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32209

Query Match          2.1%; Score 6; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 AEYGLY 240
Db 25 AEYGLY 30

RESULT 74
US-09-248-796A-27194
; Sequence 27194, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
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;; PRIOR FILING DATE: 1998-08-13  
;; NUMBER OF SEQ ID NOS: 28208  
;; SEQ ID NO 27194  
;; LENGTH: 76  
;; TYPE: PRT  
;; ORGANISM: Candida albicans  
US-09-248-796A-27194

Query Match 2.1%; Score 6; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 VLLQSL 29  
Db 36 VLLQSL 41

RESULT 75  
US-09-107-532A-5502  
; Sequence 5502, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 5502:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 78 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...78  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5502:  
US-09-107-532A-5502

Query Match 2.1%; Score 6; DB 4; Length 78;  
Best Local Similarity 100.0%; Pred.No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 NDESM 73

Db 21 NDESM 26

Search completed: June 22, 2005, 06:53:25  
Job time : 45 secs